

PN *WO9928471-A2.
XX
XX 10-JUN-1999.
XX
XX 25-NOV-1998; 98WO-US025270.
XX
XX 01-DEC-1997; 97US-0067175P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Pastan IH, Chowdhury PS;
XX
XX WPI; 1999-371123/31.
XX
XX N-PSDB; ABL57231.
XX
XX New anti-mesothelin antibodies.
XX
XX Claim 2; Fig 1; 63pp; English.
XX
XX The present sequence is the protein sequence of anti-mesothelin scFv
CC antibody SS. This single-chain antibody was produced by immunising a
CC mouse with cDNA encoding mesothelin, creating a phage library from mRNA
CC isolated from the spleen of the immunised animal, and enrichment of anti-
CC mesothelin phage over 3 rounds of panning. scFv SS is composed of a heavy
CC chain variable region (VH) joined to a light chain variable region (VL)
CC via a peptide linker. According to Kabat's classification, the VH belongs
CC to sub-group IIA and family V and the VL belongs to sub-group VI and
CC family XI. A claimed anti-mesothelin antibody binds recombinant
CC mesothelin with a dissociation constant of less than 3 x 10 power -8 M
CC and specifically binds to cells expressing mesothelin on their cell
CC surface. The antibody comprises SS scFv, the VH and VL region of SS scFv
CC or the complementarity determining regions of SS scFv. It is preferably
CC conjugated to a therapeutic agent, particularly Pseudomonas exotoxin or
CC its cytotoxic fragment. The resulting immunconjugate is used in a
CC claimed method for inhibiting the growth of a malignant cell that
CC expresses mesothelin on its cell surface, especially in mesothelioma,
CC ovarian cancer, stomach cancer or squamous cell cancer. The antibody can
CC also be used to detect mesothelin in a biological sample
XX
XX Sequence 241 AA;
SQ

Query Match 100.0%; Score 1276; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.6e-77;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOVOLQOSGPELEKPGASVKLSCKASGYSFTGYTMNWKQSHGKSLIEWIGLITPYNGASS 60
Db 1 MOVOLQOSGPELEKPGASVKLSCKASGYSFTGYTMNWKQSHGKSLIEWIGLITPYNGASS 60
QY 61 YNOKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTIVTVSS 120
Db 61 YNOKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTIVTVSS 120
QY 121 GVGSGGGGGSGGSDIELTQSPAIMASPGKVTMTCSASSSVSYMHWYQOKSGTSPKR 180
Db 121 GVGSGGGGGSGGSDIELTQSPAIMASPGKVTMTCSASSSVSYMHWYQOKSGTSPKR 180
QY 181 WIYDTSKLASGVPRFRSGSGSGNSYSLTISVVEAEDDATYYCCQWMSGYPLTFGAGTKLEI 240
Db 181 WIYDTSKLASGVPRFRSGSGSGNSYSLTISVVEAEDDATYYCCQWMSGYPLTFGAGTKLEI 240
QY 241 K 241
Db 241 K 241

RESULT 2
AAB50019 standard; protein; 241 AA.
ID AAB50019
XX
XX AAB50019;
AC
XX
DT 14-MAR-2001 (first entry)

XX
XX Antimesothelin antibody SS single-chain Fv protein.
XX
XX Mesothelin; SS antibody; single-chain Fv; scFv; cytostatic;
XX cancer therapy; ovarian cancer; mesothelioma.
XX
XX Unidentified.
XX
XX WO200073346-A1.
XX
XX 07-DEC-2000.
XX
XX 26-MAY-2000; 2000WO-US014829.
XX
XX 27-MAY-1999; 99US-0160071P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Pastan I, Chowdhury PS;
XX
XX WPI; 2001-061517/07.
XX
XX Novel polypeptides comprising mutated antimesothelin antibody heavy or
PT light chain variable region, having greater binding affinity for the
PT antigen, useful as diagnostic and therapeutic agents for ovarian cancers.
XX
XX Disclosure; Fig 1; 70pp; English.
XX
XX The present sequence is antimesothelin antibody SS single chain Fv
CC protein. This sequence was used to generate mutant antibody heavy or
CC light chain variable regions, which have 5 times higher binding affinity
CC for mesothelin antigen than the parental antibody (the present sequence).
CC The mutant proteins of the present invention have substitution(s) in the
CC complementarity determining region (CDR). Malignant cells express
CC mesothelin on their surfaces, and so the mutant proteins of the present
CC invention can be used to target immunotoxin to cells expressing
CC mesothelin on their surface i.e. malignant cells. The mutant proteins of
CC the present invention can therefore be used to treat ovarian cancers,
CC mesotheliomas, and several other types of human cancers in which the
CC cells bear the mesothelin antigen
XX
XX Sequence 241 AA;
SQ

Query Match 100.0%; Score 1276; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.6e-77;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOVOLQOSGPELEKPGASVKLSCKASGYSFTGYTMNWKQSHGKSLIEWIGLITPYNGASS 60
Db 1 MOVOLQOSGPELEKPGASVKLSCKASGYSFTGYTMNWKQSHGKSLIEWIGLITPYNGASS 60
QY 61 YNOKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTIVTVSS 120
Db 61 YNOKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTIVTVSS 120
QY 121 GVGSGGGGGSGGSDIELTQSPAIMASPGKVTMTCSASSSVSYMHWYQOKSGTSPKR 180
Db 121 GVGSGGGGGSGGSDIELTQSPAIMASPGKVTMTCSASSSVSYMHWYQOKSGTSPKR 180
QY 181 WIYDTSKLASGVPRFRSGSGSGNSYSLTISVVEAEDDATYYCCQWMSGYPLTFGAGTKLEI 240
Db 181 WIYDTSKLASGVPRFRSGSGSGNSYSLTISVVEAEDDATYYCCQWMSGYPLTFGAGTKLEI 240
QY 241 K 241
Db 241 K 241

RESULT 3
ABR62132 standard; protein; 242 AA.
ID ABR62132
XX
XX ABR62132;
AC

XX 29-AUG-2003 (first entry)
DT Single chain antibody sequence #SEQ ID 20.
XX
DE
XX Tumour; drug delivery; ligand; cancer; carcinoma; bladder; breast;
KW cervix; colorectum; lung; ovary; pancreas; prostate; stomach;
KW cholangiocarcinoma; gastric sarcoma; glioma; lymphoma; melanoma;
KW multiple myeloma; osteosarcoma; head; neck; radiation; x-ray; antibody.
XX
OS Synthetic.
XX
PN WO2003028640-A2.
XX
PD 10-APR-2003.
XX
PF 27-SEP-2002; 2002WO-US030917.
XX
PR 03-OCT-2001; 2001US-0328123P.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Hallahan DE, Qu S;
XX
DR WPI; 2003-421186/39.
XX
PT Identifying molecule that binds to irradiated tumor in a subject, by
PT exposing tumor to ionizing radiation, administering library of diverse
PT molecules and isolating library molecules from tumor to identify the
PT target.
XX
PS Claim 38; Page 107-108; 108pp; English.
XX
CC The invention relates to a method for identifying a molecule that binds
CC an irradiated tumor in a subject. The method of the invention involves
CC exposing a tumor to ionizing radiation, administering a library of
CC diverse molecules to a subject, and isolating one or more molecules of
CC the library from the tumor. The method of the invention is useful for
CC identifying a molecule that binds an irradiated tumor in a subject e.g.
CC warm-blooded vertebrate and human, and also for tumor detection. The
CC tumor is a primary or a metastasized tumor such as carcinoma of the
CC bladder, breast, cervix, colorectum, lung, ovary, pancreas, prostate,
CC stomach, cholangiocarcinoma, gastric sarcoma, glioma, lymphoma, melanoma,
CC multiple myeloma, osteosarcoma, head and neck tumor and solid tumor. The
CC method of the invention is useful for X-ray-guided delivery of a
CC therapeutic composition, a diagnostic composition or their combinations
CC to a tumor in a subject. The current sequence represents a single chain
CC antibody sequence that was identified following in vivo panning to
CC irradiated tumors. This antibody binds platelet membrane glycoprotein
CC IIB
XX
SQ Sequence 242 AA;

Query Match 80.4%; Score 1025.5; DB 6; Length 242;
Best Local Similarity 81.7%; Pred. No. 8.4e-61;
Matches 196; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
DB 3 QVQLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWKQKPGQGLEWIGYINPNDGTKY 62
QY 62 NQKFRGKATLTVDKSSSTAYMDLSTSEDSAVYFCARGYDGRGFDYWGQGTVTVSSG 121
DB 63 NEKFKGKAALTSDKSSSTAYMELSLTSEDSAVYYCARFGNYG-ALDYWGQGTITVSSG 121
QY 122 VGGSGGGSGGGSDIELTQSPAIMASPGKVTMTCSASSSVSYMHMWYQKSGTSPKRW 181
DB 122 GGGSGGGSGGGSDIELTQSPITMASPGKVTITCSASSSVSYMHMFQKPKGTPSPKPW 181
QY 182 IYDTSKLASGVPRFSGSGSGNSYSLTISVEAEDDATYYCCQWSSGYPLTFGAGTKLEIK 241
DB 182 IYGTSNLASGVPRFSGSGSGTSLTISMEAEADATYYCCQWSSYPLTFGGGTKLEIK 241

RESULT 4
ADT91209
ID ADT91209 standard; protein; 242 AA.
XX
XX ADT91209;
XX AC
DT 16-DEC-2004 (first entry)
XX
DE Single chain variable fragment (scFv) antibody #2.
XX
XX Tumour; benign intracranial meningioma; arteriovenous malformation;
KW angioma; macular degeneration; melanoma; adenocarcinoma;
KW malignant glioma; prostatic carcinoma; kidney carcinoma;
KW bladder carcinoma; pancreatic carcinoma; thyroid carcinoma;
KW lung carcinoma; colon carcinoma; rectal carcinoma; brain carcinoma;
KW liver carcinoma; breast carcinoma; ovary carcinoma; angiofibroma;
KW retrolental fibroplasia; haemangioma; Kaposi's sarcoma;
KW single chain variable fragment; scFv; antibody.
XX
OS Unidentified.
XX
XX US2004191249-A1.
XX
PN 30-SEP-2004.
XX
PD 20-OCT-2003; 2003US-00689006.
XX
PF 28-APR-2000; 2000WO-US011485.
XX
PR 09-NOV-2001; 2001US-00914605.
PR 27-SEP-2002; 2002US-00259087.
XX
XX (UYVA-) UNIV VANDERBILT.
XX
PI Hallahan DE, Mernaugh R;
XX
DR WPI; 2004-698661/68.
DR N-PSDB; ADT91208.
XX
PT Screening phage-displayed antibodies binding to radiation-inducible
PT neoantigen on cell, comprises contacting cell with antibodies, treating
PT cell with radiation, contacting cell with antibodies not binding to cell,
PT detecting bound antibody.
XX
PS Claim 4; SEQ ID NO 20; 64pp; English.
XX
XX The invention relates to a method for screening phage-displayed
CC antibodies binding to radiation-inducible neoantigen on cell. The method
CC involves contacting cell with antibodies, treating cell with radiation,
CC contacting cell with antibodies not binding to cell and detecting the
CC bound antibody. The method is useful for screening several phage-
CC displayed antibodies for an ability to bind to a radiation-inducible
CC neoantigen present on a cell, where the cell is tumour cell chosen from
CC benign intracranial meningiomas, arteriovenous malformation, angioma,
CC macular degeneration, melanoma, adenocarcinoma, malignant glioma,
CC prostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic
CC carcinoma, thyroid carcinoma, lung carcinoma, colon carcinoma, rectal
CC carcinoma, brain carcinoma, liver carcinoma, breast carcinoma, ovary
CC carcinoma, solid tumours, solid tumour metastases, angiofibromas,
CC retrolental fibroplasias, haemangiomas, Kaposi's sarcoma, head and neck
CC carcinomas and their combinations or vascular endothelial cell. The
CC present sequence is a single chain variable fragment (scFv) antibody that
CC binds to radiation-inducible neoantigens.
XX
SQ Sequence 242 AA;

Query Match 80.4%; Score 1025.5; DB 8; Length 242;
Best Local Similarity 81.7%; Pred. No. 8.4e-61;
Matches 196; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
DB 3 QVQLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWKQKPGQGLEWIGYINPNDGTKY 62

QY	62	NOKFRGKATLTVDKSSSTAYMDLSTLSEDSAVVFCARGGYDGRGFDYWGQGTTVTVSSG	121
Db	63	NEKFKGKALTSDKSSSTAYMELSLTSEDSAVVYCARFGNYG-ALDYNWGQGTTVTVSSG	121
QY	122	VGSGGGGGGGSDIELTQSPAIMASPGKEKVTMTCSASSSVSYMHVYQOKSGTSPKRW	181
Db	122	GGSGGGGGGGSDIELTQSPITMSAPGEKVTITCSASSSVSYMHVYQOKPGTSPKRW	181
QY	182	IYDTSKLASGVPGRFSGSGSGNSYSLTISVVEAEDDATYCCQQWMSGYPLTFGAGTKLEIK	241
Db	182	IYGTSLNLAGVPVRFRSGSGSGTYSLSLTISMEAEADATYCCQQWSSYPLTFGGTKLEIK	241
RESULT 5			
ID	AAB47111	standard; protein; 239 AA.	
AC	AAB47111;		
XX			
DT	04-JUN-2001	(first entry)	
XX			
DE	scFv 508F.		
XX			
KW	Human; prion protein; plaque forming disease; display vehicle; kuru; aggregating protein; amyloid plaque; brain; early onset; senility; Alzheimer's disease; late onset; pre-symptomatic; SAA amyloidosis; hereditary Icelandic syndrome; multiple myeloma; scrapie; BSE; CJD; bovine spongiform encephalopathy; Creutzfeldt-Jakob Disease; FFI; Gerstmann-Straussler-Sheinker Disease; GSS; fatal familial insomnia; antibody.		
KW			
XX			
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	Domain	1..120	
FT		/note= "Heavy chain"	
FT	Region	31..35	
FT		/label= CDR1	
FT	Region	50..66	
FT		/label= CDR2	
FT	Region	99..107	
FT		/label= CDR3	
FT	Peptide	121..133	
FT		/note= "Linker"	
FT	Domain	134..239	
FT		/note= "Light chain"	
FT	Region	157..166	
FT		/label= CDR1	
FT	Region	182..188	
FT		/label= CDR2	
FT	Region	221..229	
FT		/label= CDR3	
XX			
PN	WO200118169-A2.		
XX			
PD	15-MAR-2001.		
XX			
PF	31-AUG-2000; 2000WO-IL000518.		
XX			
PR	03-SEP-1999; 99US-0152417P.		
PR	29-DEC-1999; 99US-00473653.		
PR	31-JUL-2000; 2000US-00629971.		
XX			
PA	(UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.		
XX			
PI	Solomon B, Frenkel D, Hanan E;		
XX			
DR	WPI; 2001-244564/25.		
DR	N-PSDB; AAC85539.		
XX			
PT	Treating amyloidogenic disease such as Alzheimer's disease, BSE or CJD comprises presentation of plaque derived antigens or epitopes on a		

PT display vehicle, and introducing the vehicle into the recipient.

XX

XX

PS

XX

XX

Example 2; Fig 11, 120pp; English.

CC This sequence shows scFv 508F heavy chain, linker and light chain. The

CC scFv fragment was derived from the 508 IGM hybridoma which is generated

CC from splenocytes of a mouse that has been immunised with a peptide

CC corresponding to the 16 amino terminal residues of beta-AP conjugated to

CC keyhole limpet hemocyanin used a carrier. The resultant variable chain

CC fragments may be used in the method of the invention. Cys 96 of the VL

CC fragment was replaced with various amino acids to see if production yield

CC or stability were effected without having an adverse effect on its

CC binding affinity. The invention provides an agent for treating a plaque

CC forming disease. Antigenic polypeptides are displayed on a display

CC vehicle and are capable of eliciting antibodies capable of disaggregating

CC the aggregating protein and/or of preventing aggregation of the

CC aggregating protein. This reduces formation of amyloid plaques in the

CC brain of victims of plaque forming diseases, e.g. early onset Alzheimer's

CC disease, late onset Alzheimer's disease, pre-symptomatic Alzheimer's

CC disease, SAA amyloidosis, hereditary Icelandic syndrome, senility,

CC multiple myeloma, scrapie, bovine spongiform encephalopathy (BSE), kuru,

CC Creutzfeldt-Jakob Disease (CJD), Gerstmann-Strausler-Sheinker Disease

CC (GSS) and fatal Familial insomnia (FFI)

XX

XX

Sequence 239 AA;

[illegible]

RESULT	6
AA016066	
ID	AA016066 standard; protein; 239 AA.
XX	
AC	AA016066;
XX	
DT	27-FEB-2003 (first entry)
XX	
DE	Human neurological/CNS disease treatment method-related protein.
XX	
KW	Vaccine; gene therapy; neurological disease; CNS disorder;
KW	central nervous system disorder; olfactory system; Alzheimer's disease;
KW	Creutzfeldt-Jakob disease; Huntington's chorea; Parkinson's disease;
KW	viral infection of the brain; brain tumour; lysosomal storage disease;
KW	multiple sclerosis.
XX	
OS	Homo sapiens.
XX	
PN	WO200274243-A2.
XX	
PD	26-SEP-2002.
XX	

PF 15-MAR-2002; 2002WO-US008042.
XX
PR 15-MAR-2001; 2001US-00808037.
XX
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA (MCIN/) MCINNIS P.
XX
PI Solomon B, Frenkel D;
XX
XX WPI; 2003-040542/03.
DR N-PSDB; AAL51099.
XX
PT Treating or diagnosing neurological diseases of the central nervous
PT system, e.g. Alzheimer's disease, comprises displaying a polypeptide or
PT diagnostic agent on viral display vehicle and introducing or detecting
PT the display vehicle.
XX
XX
PS Example 2; Fig 11A; 214pp; English.
XX
XX The invention comprises a method for treating a neurological disease or a
CC central nervous system (CNS) disorder. The method involves displaying a
CC therapeutic molecule capable of treating the neurological disease or CNS
CC disorder on a viral display vehicle. The viral display vehicle is then
CC introduced into the olfactory system of a subject to treat the disease or
CC disorder. The method of the invention is useful for preventing, treating
CC and diagnosing neurological diseases or CNS disorders, such as:
CC Alzheimer's disease; Creutzfeld-Jakob disease; Huntington's chorea; viral
CC infections of the brain; brain tumours; lysosomal storage diseases;
CC Parkinson's disease; and multiple sclerosis. The present amino acid
CC sequence represents a protein which was used in the invention
XX
SQ Sequence 239 AA;

```

Query Match      79.2%; Score 1010.5; DB 6; Length 239;
Best Local Similarity 79.8%; Pred. No. 8.3e-60;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2

OY    2 QVQLQDQSPELEKPGASVKLSCKRAGSYFTGYTMNWVKQSHGSKLEWIGLITPYNCASSY 61
      ||::||| : || |::||| ::||| : ||| : |||
DB    1 QVKIQESGAELVRPGVSVKISCKSGGYFTTDYAMHWVKQSHAKSLIEWIGVISTYYGDASY 60

OY    62 NQKFRGKATLTVDKSSSTAYMDLLSITSEDAVAVFCARG--GYDGRGPDYWGCGTIVTV 118
      ||::||| : ||| ::||| : ||| : ||| : |||
DB    61 NQKFKGKATMTVDKSSSTAYMELARLTSEDAIYYCARGATMSY----FDYWGVTTVTV 116

OY    119 SSGVGSGSGGGSGGGSDIELTQSPAIMSASPGEKYMTCSASSSVYMHWYQQKSGTSP 178
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB    117 SSGGGSGSGVGSGGGGSDELTLQSPAIMSASPGEKYMTCSASSSI SYMHMWYQQKPGTSP 176

OY    179 KRWIYDTSKLASGVPRFSGSGSGNSYSLTISSVEAEDDATYYCCQMSGYPPLTFGAGTKL 238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB    177 KRWIYDTSKLASGVPARFSGSGSGTSYSTLTSSMEAEADATYYCHQRSSYPPTFGGAKL 236

OY    239 EIK 241
      |||
DB    237 EIK 239

RESULT 7
ADJ88113
ID ADJ88113 standard; protein; 239 AA.

XX AC ADJ88113;
XX DT 06-MAY-2004 (first entry)
DE Human beta amyloid peptide antibody (508) heavy chain protein.
XX KM Neurological disease; central nervous system; CNS disorder;
KM plaque-forming disease; Alzheimer's disease; SAA amyloidosis;
KM hereditary icteric syndrome; senility; multiple myeloma; scrapie;
KM bovine spongiform encephalopathy; BSE; kuru; Creutzfeldt-Jakob disease;
KM CJD; Gerstmann-Strauszler-Sheinker disease; GSS; fatal familial insomnia;

```

XX FFI; non-plaque-forming disease; Huntington's chorea; viral infection;
 KW brain tumour; lysosomal storage disease; neurodegeneration;
 KW multiple sclerosis; vaccine; beta amyloid peptide; beta AP; antibody;
 KW human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 31. .35
 FT /note= "CDR1"
 FT Region 50. .66
 FT /note= "CDR2"
 FT Region 99. .107
 FT /note= "CDR3"
 XX
 PN US2004013647-A1.
 XX
 PD 22-JAN-2004.
 XX
 PF 11-MAR-2003; 2003US-00384788.
 XX
 PR 03-SEP-1999; 99US-0152417P.
 PR 29-DEC-1999; 99US-00473653.
 PR 31-JUL-2000; 2000US-00629971.
 PR 31-AUG-2000; 2000WO-11000518.
 PR 15-MAR-2001; 2001US-00808037.
 PR 07-AUG-2001; 2001US-00830954.
 PR 12-APR-2002; 2002US-0371735P.
 PR 06-JUN-2002; 2002US-00162889.
 XX
 PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
 XX
 PI Solomon B, Frenkel D;
 XX
 DR WPI; 2004-108188/11.
 DR N-PSDB; ADJ88112.
 XX
 PT Treating neurological disease CNS e.g., Alzheimer's disease, by
 PT displaying therapeutic molecule capable of treating the disease on viral
 PT display vehicle which is then administered to subject through olfactory
 PT system.
 XX
 PS Example 2; SEQ ID NO 6; 68pp; English.
 PS
 XX
 CC The invention relates to a method of treating a neurological disease or
 CC disorder of the central nervous system (CNS). The method involves
 CC displaying a therapeutic molecule capable of treating the neurological
 CC disease or disorder of the CNS on a viral display vehicle and introducing
 CC viral display vehicle into a subject by applying an effective amount of
 CC the viral display vehicle displaying the therapeutic molecule to an
 CC olfactory system of the subject. The method is useful for treating a
 CC neurological disease or disorder of CNS such as a plaque-forming disease
 CC such as Alzheimer's disease, late onset Alzheimer's disease,
 CC presymptomatic Alzheimer's disease, SAA amyloidosis, hereditary Icelandic
 CC syndrome, senility, multiple myeloma, scrapie, bovine spongiform
 CC encephalopathy (BSE), kuru, Creutzfeldt-Jakob disease (CJD), Gerstmann-
 CC Streussler-Sheinker disease (GSS) or fatal familial insomnia (FFI). The
 CC method is also useful for treating a non plaque forming disease or
 CC disorder e.g. Huntington's chorea, viral infections of the brain, brain
 CC tumours, lysosomal storage diseases which cause neurodegeneration and are
 CC manifested by enzyme deficiencies and multiple sclerosis. The invention
 CC is also used in the preparation of vaccines. The present sequence is
 CC human beta amyloid peptide (beta AP) antibody heavy chain protein. This
 CC sequence is used to illustrate the method of the invention.
 XX
 SQ Sequence 239 AA;

Query Match	79.2%;	Score 1010.5;	DB 8;	Length 239;
Best Local Similarity	79.8%;	Pred. No. 8.3e-60;		
Matches 194;	Conservative 16;	Mismatches 26;	Indels 7;	Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGTYMNWVKOSHGSLEWIGLITPNGASSY 61

CC modulating a CA 125 tumour antigen in a mammalian cell. Also described:
CC (1) a recombinant nucleic acid comprising at least one sequence selected
CC from the group consisting of ADC79233, ADC79234, ADC79235, ADC79236,
CC ADC79237 and ADC79238; (2) a vector comprising the recombinant nucleic
CC acid; (3) a host cell; (4) a pharmaceutical composition; (5) preventing
CC or treating CA 125 tumour antigen-associated disease in a mammal; and (6)
CC negatively modulating a CA 125 tumour antigen in a mammalian cell. A
CC modulator capable of negatively modulating a CA 125 tumour antigen has
CC cytostatic activity, and can be used in gene therapy. The modulator,
CC recombinant nucleic acid, vector or host cell can be used for preparing a
CC composition for preventing or treating CA 125 tumour antigen-associated
CC disease in a mammal. The present sequence is used in the exemplification
CC of the present invention.

XX
SQ Sequence 239 AA;

Query Match 78.3%; Score 998.5; DB 7; Length 239;
Best Local Similarity 79.4%; Pred. No. 5.3e-59;
Matches 193; Conservative 14; Mismatches 29; Indels 7; Gaps 2;

Oy 2 QVQLQSGPELEKPGASVKLSCKASGYFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
Db 1 QVQLQESGPELVKPGASVKISCKASGYFTFDYNMHWKQSHGKSLEWIGYIYPYNGDTGY 60
Oy 62 NQFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARGG---YDGRGFDYWGQGTITV 118
Db 61 NQFRNKASLTVDTSSTAYMELRLSTSEDSAVYYWARSGFMY---FDVWGQGTITV 116
Oy 119 SSGVGGSGGGGGGGSDIELTQSPAIMSAPGEKVTMTCSASSSVSYMHYQOKSGTSP 178
Db 117 SSGGGSGGGGGGGGSDIQMTQSPAILSASPEKVTMTCRATPSVSYMHYQOKPGSSP 176
Oy 179 KRMIYDTSKILASGVPRFSGSGSGNSYSLTISVVEAEDDATYYCQQWSGYPLTFGAGTKL 238
Db 177 KPWITYTTSNLASGVPARFSGSGSGTSYSLTVSRVEAEDATYYCQQWSRSPPTFGAGAKL 236
Oy 239 EIK 241
Db 237 EIK 239

RESULT 10
ADC79231
ID ADC79231 standard; protein; 239 AA.
XX
AC ADC79231;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-CA125 scFvs VK-8-1.9 amino acid sequence.
XX
KW CA 125 tumour antigen; CA 125 tumour antigen modulator;
KW CA 125 tumour antigen-associated disease; cytostatic; gene therapy.
XX
OS Synthetic.
XX
PN WO2003076465-A2.
XX
PD 18-SEP-2003.
XX
PE 11-MAR-2003; 2003WO-CA000341.
XX
PR 11-MAR-2002; 2002US-0363306P.
PR 28-FEB-2003; 2003CA-02420494.
XX
PA (UYSH) UNIV SHERBROOKE.
XX
PI Rancourt C, Piche A, Beaudin J;
XX
DR WPI; 2003-722323/68.
PT New modulator capable of negatively modulating a CA 125 tumor antigen in
PT a mammalian cell, useful for preparing a composition for preventing or

PT treating CA 125 tumor antigen-associated disease in a mammal.
XX
XX Disclosure; Fig 29C; 90pp; English.
XX

CC The present invention describes a modulator capable of negatively
CC modulating a CA 125 tumour antigen in a mammalian cell. Also described:
CC (1) a recombinant nucleic acid comprising at least one sequence selected
CC from the group consisting of ADC79233, ADC79234, ADC79235, ADC79236,
CC ADC79237 and ADC79238; (2) a vector comprising the recombinant nucleic
CC acid; (3) a host cell; (4) a pharmaceutical composition; (5) preventing
CC or treating CA 125 tumour antigen-associated disease in a mammal; and (6)
CC negatively modulating a CA 125 tumour antigen in a mammalian cell. A
CC modulator capable of negatively modulating a CA 125 tumour antigen has
CC cytostatic activity, and can be used in gene therapy. The modulator,
CC recombinant nucleic acid, vector or host cell can be used for preparing a
CC composition for preventing or treating CA 125 tumour antigen-associated
CC disease in a mammal. The present sequence is used in the exemplification
CC of the present invention.

XX
SQ Sequence 239 AA;

Query Match 78.2%; Score 997.5; DB 7; Length 239;
Best Local Similarity 79.4%; Pred. No. 6.2e-59;
Matches 193; Conservative 14; Mismatches 29; Indels 7; Gaps 2;

Oy 2 QVQLQSGPELEKPGASVKLSCKASGYFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
Db 1 QVQLQESGPELVKPGASVKISCKASGYFTFDYNMHWKQSHGKSLEWIGYIYPYNGDTGY 60
Oy 62 NQFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARGG---YDGRGFDYWGQGTITV 118
Db 61 NQFRNKASLTVDTSSTAYMELRLSTSEDSAVYYCARSGFMY---FDVWGQGTITV 116
Oy 119 SSGVGGSGGGGGGGSDIELTQSPAIMSAPGEKVTMTCSASSSVSYMHYQOKSGTSP 178
Db 117 SSGGGSGGGGGGGGSDIQMTQSPAILSASPEKVTMTCRATPSVSYMHYQOKPGSSP 176
Oy 179 KRMIYDTSKILASGVPRFSGSGSGNSYSLTISVVEAEDDATYYCQQWSGYPLTFGAGTKL 238
Db 177 KPLIYTTSNLASGVPARFSGSGSGTSYSLTVSRVEAEDATYYCQQWSRSPPTFGAGTKL 236
Oy 239 EIK 241
Db 237 EIK 239

RESULT 11
AAR79872
ID AAR79872 standard; protein; 242 AA.
XX
AC AAR79872;
XX
DT 02-JUL-1996 (first entry)
XX
DE Anti-EGFR single chain antibody (Clone 11 H 1).
XX
KW Single chain antibody; antibody; epidermal growth factor receptor; EGFR;
KW tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment;
KW phage antibody library.
XX
OS Mus musculus.
XX
PN WO9525167-A1.
XX
PD 21-SEP-1995.
XX
PE 16-MAR-1995; 95WO-EP000978.
XX
PR 17-MAR-1994; 94EP-00104160.
PR 02-DEC-1994; 94EP-00118970.
XX
PA (MERE) MERCK PATENT GMBH.
XX

PI Kettleborough AC, Bendig MM, Ansell KH, Guessow D, Adan J;
PI Mltjans F, Rosell E, Blasco F, Piulats J;
XX
XX WPI; 1995-336972/43.
DR N-PSDB; AAT04025.
XX
PT Anti-EGFR antibodies and single chain Fv antibody fragments - obtained
PT from phage-antibody libraries, useful for diagnosis and therapy of
PT tumours.
XX
PS Claim 4; Page 72-73; 93pp; English.
XX
CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies and
CC antibodies constructed from anti-EGFR antibody fragments can be used for
CC diagnosis of tumours and assessment of tumour growth in vitro and in
CC vivo. They may also be used in a pharmaceutical composition for the
CC therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and
CC fragments are derived from mice but are humanised so as to cause minimum
CC reaction against them. They are produced using the phage antibody
CC library. They are produced using the phage antibody library. (See
CC AAT04011-T04026 and AAR79858-R79873)
XX
SQ Sequence 242 AA;

Query Match 78.0%; Score 995; DB 2; Length 242;
Best Local Similarity 79.8%; Pred. No. 9.2e-59;
Matches 193; Conservative 17; Mismatches 30; Indels 2; Gaps 1;
QY 2 QVQLQSGPELEKPGASVKLSCKASGYFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
Db 1 EVQLQSGAELVKGASVKLSCKASGYFTTSHMMHWKQRAQGGLIEWIGEFNPSNGRTNY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARG--GYDGRGFDYWGQGTITVVS 119
Db 61 NEKFKSKATLTVDKSSSTAYMQLSLTSEDSAVYYCASRDYDGRYFDYWGQGTITVVS 120
QY 120 SGVGGSGGGSGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHVYQOKSGTSPK 179
Db 121 SGGGSGGGSGGGSDIELTQSPISMSASPGKVTMTCSASSSVSYMYWYQOKTSSPR 180
QY 180 RWIYDTSKLASGVPRFSGSGSGNSYSLTISVYEADDDATYYCQWMSGYP-PLTFGAGTKLE 239
Db 181 LLIYDTSNLASGVPRFSGSGSGTSLTISRMEADDAATYYCQWMSGYPHTFGAGTKLE 240
QY 240 IK 241
Db 241 IK 242

RESULT 12
AAR79867
ID AAR79867 standard; protein; 244 AA.
XX
AC AAR79867;
XX
DT 02-JUL-1996 (first entry)
XX
DE Anti-EGFR single chain antibody (Clone 10 D 2).
XX
KW Single chain antibody; antibody; epidermal growth factor receptor; EGFR;
KW tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment;
KW phage antibody library.
XX
OS Mus musculus.
XX
PN W09525167-A1.
XX
PD 21-SEP-1995.
XX
PF 16-MAR-1995; 95WO-EP000978.
XX
PR 17-MAR-1994; 94EP-00104160.
PR 02-DEC-1994; 94EP-00118970.
XX

XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Kettleborough AC, Bendig MM, Ansell KH, Guessow D, Adan J;
PI Mltjans F, Rosell E, Blasco F, Piulats J;
XX
XX WPI; 1995-336972/43.
DR N-PSDB; AAT04020.
XX
PT Anti-EGFR antibodies and single chain Fv antibody fragments - obtained
PT from phage-antibody libraries, useful for diagnosis and therapy of
PT tumours.
XX
PS Claim 4; Page 60-61; 93pp; English.
XX
CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies and
CC antibodies constructed from anti-EGFR antibody fragments can be used for
CC diagnosis of tumours and assessment of tumour growth in vitro and in
CC vivo. They may also be used in a pharmaceutical composition for the
CC therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and
CC fragments are derived from mice but are humanised so as to cause minimum
CC reaction against them. They are produced using the phage antibody
CC library. They are produced using the phage antibody library. (See
CC AAT04011-T04026 and AAR79858-R79873)
XX
SQ Sequence 244 AA;

Query Match 77.8%; Score 993; DB 2; Length 244;
Best Local Similarity 79.9%; Pred. No. 1.3e-58;
Matches 195; Conservative 14; Mismatches 31; Indels 4; Gaps 2;
QY 2 QVQLQSGPELEKPGASVKLSCKASGYFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
Db 1 EVQLQSGAELVKGASVKLSCKASGYFTTSHMMHWKQRAQGGLIEWIGEFNPSNGRTNY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARG--GYDGRGFDYWGQGTITVVS 119
Db 61 NEKFKSKATLTVDKSSSTAYMQLSLTSEDSAVYYCASRDYDGRYFDYWGQGTITVVS 120
QY 120 SGVGGSGGGSGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHVYQOKSGTSPK 179
Db 121 SGGGSGGGSGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMYWYQOKRPGSSPR 180
QY 180 RWIYDTSKLASGVPRFSGSGSGNSYSLTISVYEADDDATYYCQWMSGYP--LTFGAGTK 237
Db 181 LLIYDTSNLASGVPRFSGSGSGTSLTISRMEADDAATYYCQWMSGYPMTYFGGGTK 240
QY 238 LEIK 241
Db 241 LEIK 244

RESULT 13
ABR62131
ID ABR62131 standard; protein; 242 AA.
XX
AC ABR62131;
XX
DT 29-AUG-2003 (first entry)
XX
DE Single chain antibody amino acid sequence #SEQ ID 18.
XX
KW Tumour; drug delivery; ligand; cancer; carcinoma; bladder; breast;
KW cervix; colorectum; lung; ovary; pancreas; prostate; stomach;
KW cholangiocarcinoma; gastric sarcoma; glioma; lymphoma; melanoma;
KW multiple myeloma; osteosarcoma; head; neck; radiation; antibody.
XX
OS Synthetic.
XX
PN W02003028640-A2.
XX
PD 10-APR-2003.
XX

PF 27-SEP-2002; 2002WO-US030917.
XX
PR 03-OCT-2001; 2001US-0328123P.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Hallahan DE, Qu S;
XX
DR WPI; 2003-421186/39.
DR N-PSDB; ACC83314.
XX
PT Identifying molecule that binds to irradiated tumor in a subject, by
PT exposing tumor to ionizing radiation, administering library of diverse
PT molecules and isolating library molecules from tumor to identify the
PT target.
XX
PS Claim 38; Page 105-106; 108pp; English.
XX
CC The invention relates to a method for identifying a molecule that binds
CC an irradiated tumor in a subject. The method of the invention involves
CC exposing a tumor to ionizing radiation, administering a library of
CC diverse molecules to a subject, and isolating one or more molecules of
CC the library from the tumor. The method of the invention is useful for
CC identifying a molecule that binds an irradiated tumor in a subject e.g.
CC warm-blooded vertebrate and human, and also for tumor detection. The
CC tumor is a primary or a metastasized tumor such as carcinoma of the
CC bladder, breast, cervix, colorectum, lung, ovary, pancreas, prostate,
CC stomach, cholangiocarcinoma, gastric sarcoma, glioma, lymphoma, melanoma,
CC multiple myeloma, osteosarcoma, head and neck tumor and solid tumor. The
CC method of the invention is useful for X-ray-guided delivery of a
CC therapeutic composition, a diagnostic composition or their combinations
CC to a tumor in a subject. The current sequence represents a single chain
CC antibody sequence that was identified following in vivo panning to
CC irradiated tumours. This antibody binds P-selectin
XX
SQ Sequence 242 AA;

Query Match 77.5%; Score 989.5; DB 6; Length 242;
Best local Similarity 80.4%; Pred. No. 2.1e-58;
Matches 193; Conservative 14; Mismatches 32; Indels 1; Gaps 1;

QY 2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMWVKQSHGKSLIEWIGLITPYNGASSY 61
DB 3 QVQLQQSGAELVMPGASVKMSCKASGYFTFDYWMHWKQRPQGLEWIGALDTSYSTSY 62
QY 62 NQFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTIVTVSSG 121
DB 63 NQFRGKATLTVDSSSTAYMQLSLTSEDSAVVYCARRGYS-AFDYWGQGTIVTVSSG 121
QY 122 VGGSGGGSGGGSDIELTQSPALMSASPGKVTMTCSASSSVSYMHVYQKSGTSPKRW 181
DB 122 GGGSGGGSGGGSDIELTQSPPTMAASPGKVTITCRASSSVSYMHWFQKSGTSPKRW 181
QY 182 IYDTSKLASGVPRFSSGSGNSYSLTISSEAEADATYYCCQWSGYPLTFGAGTKLEIK 241
DB 182 IYDTSKLASGVPRFSSGSGSGTYSLTISSEAEADATYYCLQRSSYPYTFGAGTKLEIK 241

RESULT 14
ADT91207
ID ADT91207 standard; protein; 242 AA.
XX
AC ADT91207;
XX
DT 16-DEC-2004 (first entry)
XX
DE Single chain variable fragment (scFv) antibody #1.
XX
KW Tumour; benign intracranial meningioma; arteriovenous malformation;
KW angioma; macular degeneration; melanoma; adenocarcinoma;
KW malignant glioma; prostatic carcinoma; kidney carcinoma;
KW bladder carcinoma; pancreatic carcinoma; thyroid carcinoma;
KW lung carcinoma; colon carcinoma; rectal carcinoma; brain carcinoma;

KW liver carcinoma; breast carcinoma; ovary carcinoma; angiofibroma;
KW retrolental fibroplasia; haemangioma; Kaposi's sarcoma;
KW single chain variable fragment; scFv; antibody.
XX
OS Unidentified.
XX
PN US2004191249-A1.
XX
PD 30-SEP-2004.
XX
PF 20-OCT-2003; 2003US-00689006.
XX
PR 28-APR-2000; 2000WO-US011485.
PR 09-NOV-2001; 2001US-00914605.
PR 27-SEP-2002; 2002US-00259087.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Hallahan DE, Mernaugh R;
XX
DR WPI; 2004-698661/68.
DR N-PSDB; ADT91206.
XX
PT Screening phage-displayed antibodies binding to radiation-inducible
PT neoantigen on cell, comprises contacting cell with antibodies, treating
PT cell with radiation, contacting cell with antibodies not binding to cell,
PT detecting bound antibody.
XX
PS Claim 4; SEQ ID NO 18; 64pp; English.
XX
CC The invention relates to a method for screening phage-displayed
CC antibodies binding to radiation-inducible neoantigen on cell. The method
CC involves contacting cell with antibodies, treating cell with radiation,
CC contacting cell with antibodies not binding to cell and detecting the
CC bound antibody. The method is useful for screening several phage-
CC displayed antibodies for an ability to bind to a radiation-inducible
CC neoantigen present on a cell, where the cell is tumour cell chosen from
CC benign intracranial meningiomas, arteriovenous malformation, angioma,
CC macular degeneration, melanoma, adenocarcinoma, malignant glioma,
CC prostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic
CC carcinoma, thyroid carcinoma, lung carcinoma, colon carcinoma, rectal
CC carcinoma, brain carcinoma, liver carcinoma, breast carcinoma, ovary
CC carcinoma, solid tumours, solid tumour metastases, angiofibromas,
CC retrolental fibroplasias, haemangiomas, Kaposi's sarcoma, head and neck
CC carcinomas and their combinations or vascular endothelial cell. The
CC present sequence is a single chain variable fragment (scFv) antibody that
CC binds to radiation-inducible neoantigens.
XX
SQ Sequence 242 AA;

Query Match 77.5%; Score 989.5; DB 8; Length 242;
Best local Similarity 80.4%; Pred. No. 2.1e-58;
Matches 193; Conservative 14; Mismatches 32; Indels 1; Gaps 1;

QY 2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMWVKQSHGKSLIEWIGLITPYNGASSY 61
DB 3 QVQLQQSGAELVMPGASVKMSCKASGYFTFDYWMHWKQRPQGLEWIGALDTSYSTSY 62
QY 62 NQFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTIVTVSSG 121
DB 63 NQFRGKATLTVDSSSTAYVQLSLTSEDSAVVYCARRGYS-AFDYWGQGTIVTVSSG 121
QY 122 VGGSGGGSGGGSDIELTQSPALMSASPGKVTMTCSASSSVSYMHVYQKSGTSPKRW 181
DB 122 GGGSGGGSGGGSDIELTQSPPTMAASPGKVTITCRASSSVSYMHWFQKSGTSPKRW 181
QY 182 IYDTSKLASGVPRFSSGSGNSYSLTISSEAEADATYYCCQWSGYPLTFGAGTKLEIK 241
DB 182 IYDTSKLASGVPRFSSGSGSGTYSLTISSEAEADATYYCLQRSSYPYTFGAGTKLEIK 241

RESULT 15
AAR79870

A;Residues: 1-137 <KOF>
A;Cross-references: GB:M20831; NID:g196949; PIDN:AAA38848.1; PID:g196950
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 40.2%; Score 513.5; DB 2; Length 137;
Best Local Similarity 82.4%; Pred. No. 1.8e-27;
Matches 98; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EIQLQSGAELVKPGASVKISCKASGYSFTGYTMNWVKQSHGKSLIEWIGININPYGSTSY 79
QY 62 NQKFRGKATLTVDKSSSTAYMDLSLTSEDSAVYFCARGGYDGRGFDYWGQGTITVSS 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFRGKATLTVDKSSSTAYMDLSLTSEDSAVYVCARKNY-GSSFDYWGQGTITVSS 137

RESULT 7

E45722
anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 5) - mouse (fr
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: E45722
R;Simson, J.A.; Chow, J.C.; Baker, J.; Avdaloovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A;Reference number: A45722; MUID:93100833; PMID:7677958
A;Accession: E45722
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-120 <SIM>
A;Note: sequence extracted from NCBI backbone (NCBIP:120593)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 39.5%; Score 503.5; DB 2; Length 120;
Best Local Similarity 79.2%; Pred. No. 7.3e-27;
Matches 95; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGL-ITPYNGASS 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLQSGPELVKPGASMKISCKASYSFTGYTMNWVKQSHGQNLIEWIGLIINPYNGCTS 60
QY 61 YNOKFRGKATLTVDKSSSTAYMDLSLTSEDSAVYFCARGGYDGRGFDYWGQGTITVSS 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YNOKFRGKATLTVDKSSNTAYMELSLTSADSAVYCTRRGFRDYSMDYWGQGTITVSS 120

RESULT 8

JL0079
Ig kappa chain precursor V region (anti-phenylloxazalone 6F6) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C;Accession: JL0079; A49044; B49044
R;Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988
A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-rea
A;Reference number: JL0076; MUID:89096973; PMID:3211160
A;Accession: JL0079
A;Molecule type: mRNA
A;Residues: 1-130 <KAA>
A;Cross-references: GB:M27792; NID:g197159
A;Experimental source: mRNA clones for anti-phenylloxazalone antibody 6F6
A;Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10
A;Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation
R;Mlstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.
Eur. J. Immunol. 22, 1627-1634, 1992
A;Title: Non-random features of the repertoire expressed by the members of one V kappa g
A;Reference number: A49044; MUID:92289826; PMID:1601044
A;Accession: A49044

A;Molecule type: DNA
A;Residues: 1-25 <MIL>
A;Cross-references: GB:S37663; NID:g250214; PIDN:AAB22331.1; PID:g250217
A;Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBIP:106809)
A;Accession: B49044
A;Molecule type: DNA
A;Residues: 114-116 <MIL2>
A;Cross-references: GB:S37664; NID:g250215; PIDN:AAB22332.1; PID:g250218
A;Experimental source: BALB/c germ-line
A;Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addi
C;Genetics:
A;Gene: V(kappa)Ox1
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
F;38-111/Domain: immunoglobulin homology <IMM>
F;45-109/Disulfide bonds: #status predicted

Query Match 39.3%; Score 502; DB 1; Length 130;
Best Local Similarity 92.4%; Pred. No. 1e-26;
Matches 97; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 137 IELTQSPAIMSAPGEKVTMTCSASSSVSYMHVQOKSGTSPKRWIYDTSKLASGVPGRF 196
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 24 IVLTSPAIMSASGEKVTMTCSASSSVSYMHVQOKSGTSPKRWIYDTSKLASGVPARF 83
QY 197 SGSGSGNSYSLTITSSVEABDDATYYCQQWSGYPLTFGAGTKLEIK 241
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 84 SGSGSGXSYSLTITSSMEABDDATYYCQQWSNPLTFGAGTKLEIK 128

RESULT 9

F30502
Ig heavy chain V region (A52) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C;Accession: F30502
R;Elat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mic
A;Reference number: A30502; MUID:88315787; PMID:2457627
A;Accession: F30502
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <EIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 39.3%; Score 501.5; DB 2; Length 119;
Best Local Similarity 78.9%; Pred. No. 9.8e-27;
Matches 97; Conservative 9; Mismatches 8; Indels 9; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIQLQSGAELVKPGASVKISCKASGYSFTGYTMNWVKQSHGKSLIEWIGININPYGSTSY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLSLTSEDSAVYFCA-----RGGYDGRGFDYWGQGTITV 116
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFRGATLTVDKSSSTAYMDLSLTSEDSAVYVCARGRLRRGCY-----FDYWGQGTITL 116
QY 117 TVSS 119
|||
Db 117 TVSS 119

RESULT 10

PH0099

Ig heavy chain V region (anti-cyclosporin F) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
C/Accession: PH0099
R/Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; V
Mol. Immunol. 27, 1029-1038, 1990
A/Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
A/Reference number: PH0087; MUID:91042649; PMID:2122240
A/Accession: PH0099
A/Molecule type: mRNA
A/Residues: 1-119 <SCH>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>
F/31-35/Region: complementarity-determining 1
F/50-66/Region: complementarity-determining 2
F/99-106/Region: complementarity-determining 3

Query Match 39.3%; Score 501; DB 2; Length 119;
Best Local Similarity 80.7%; Pred. No. 1.1e-26;
Matches 96; Conservative 11; Mismatches 10; Indels 2; Gaps 1;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKOSHGKSLIEWIGLITPYNGASSY 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLQSGPELVPEPGASVKISKASGYSFAGYTMWVKOSHGNLEWIGLINPYDGIAT 60

QY 62 NQKFRKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTIVTVSS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFKKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGYY--YAVDYWGQGTIVTVSS 117

RESULT 11
S26319
Ig heavy chain V region - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C/Accession: S26319
R/Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A/Title: Antibodies that are specific for a single amino acid interchange in a protein e
A/Reference number: S26309; MUID:91341421; PMID:1908510
A/Accession: S26319
A/Molecule type: mRNA
A/Residues: 1-114 <STA>
A/Cross-references: EMBL:X59172
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/11-94/Domain: immunoglobulin homology <IMM>

Query Match 39.2%; Score 500.5; DB 2; Length 114;
Best Local Similarity 82.6%; Pred. No. 1.1e-26;
Matches 95; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

QY 6 QQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKOSHGKSLIEWIGLITPYNGASSYQKF 65
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QQSGPELVKPGASVKISKASGYSFTGYFMNWVKOSHGKSLIEWIGRINPYNGDTFYNQKF 60

QY 66 RKGATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTIVTVSS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 KKGATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYG-AMDYWGQGTIVTVSS 114

RESULT 12
S29591
Ig kappa chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S29591
R/Kavaler, J.
submitted to the EMBL Data Library, April 1991
A/Reference number: S26459
A/Accession: S29591
A/Status: preliminary

A/Molecule type: mRNA
A/Residues: 1-103 <KAV>
A/Cross-references: EMBL:X59094; NID:G52227; PIDN:CAA41820.1; PID:G52228
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-88/Domain: immunoglobulin homology <IMM>

Query Match 39.1%; Score 499; DB 2; Length 103;
Best Local Similarity 93.2%; Pred. No. 1.2e-26;
Matches 96; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 137 IELTQSPAIMASPEKVTMTCSASSSVSYMHYQOKSGTSPKRWIYDTSKLASGVPGRF 196
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 IVLTSIPAIMASPEKVTMTCSASSSVSYMHYQOKSGTSPKRWIYDTSKLASGVPARF 60

QY 197 SGSGSGNSYSLTISVEAEDDATYYCQQWSGYPLTFGAGTKLE 239
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGSGSGTYSYLTISMEADAATYYCQQWSNPLYTFGAGTKLE 103

RESULT 13
A30562
Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C/Accession: A30562
R/Sikder, S.K.; Borden, P.; Gruzo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
J. Immunol. 142, 888-893, 1989
A/Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bir
A/Reference number: A30562; MUID:89110066; PMID:2464031
A/Accession: A30562
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-107 <SIK>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-89/Domain: immunoglobulin homology <IMM>

Query Match 39.1%; Score 499; DB 2; Length 107;
Best Local Similarity 91.4%; Pred. No. 1.3e-26;
Matches 96; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 137 IELTQSPAIMASPEKVTMTCSASSSVSYMHYQOKSGTSPKRWIYDTSKLASGVPGRF 196
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 IVLTSIPAIMASPEKVTMTCSASSSVSYMHYQOKSGTSPKRWIYDTSKLASGVPARF 61

QY 197 SGSGSGNSYSLTISVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 SGSGSGTYSYLTISMEADAATYYCQQWSNPLYTFGGTKLEIK 106

RESULT 14
F45722
anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 33) - mouse (fr
C/Species: Mus musculus (house mouse)
C/Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C/Accession: F45722
R/Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasque
J. Virol. 67, 489-496, 1993
A/Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A/Reference number: A45722; MUID:93100833; PMID:7677958
A/Accession: F45722
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-120 <SIM>
A/Note: sequence extracted from NCBI backbone (NCBIP:120594)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: glycoprotein
F/15-99/Domain: immunoglobulin homology <IMM>

Query Match 38.9%; Score 496.5; DB 2; Length 120;
Best Local Similarity 78.3%; Pred. No. 2.1e-26;
Matches 94; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 24, 2005, 18:38.13 ; Search time 169 Seconds
(without alignments)
730.243 Million cell updates/sec

Title: US-09-979-539-1
Perfect score: 1276
Sequence: 1 MQVQLQSGPELEKPGASVK.....CQQWSGYPLTFGAGTKLEIK 241

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	792.5	62.1	243	2 Q7TQM2	Q7Tqm2 mus musculu
2	783.5	61.4	244	2 Q65ZC8	Q65zc8 homo sapien
3	771.5	60.5	487	2 Q65ZL2	Q65z12 mus sp. fv/
4	733.5	57.5	255	2 Q6KB05	Q6kb05 mus musculu
5	726.5	56.9	241	2 Q921A6	Q921a6 mus musculu
6	720	56.4	298	2 Q9QYF0	Q9qyf0 sythetic c
7	718.5	56.3	240	2 Q65ZC9	Q65zc9 homo sapien
8	645	50.5	248	2 Q65Z07	Q65zq7 mus sp. b3(
9	628	49.2	218	2 Q925S1	Q925s1 mus musculu
10	543	42.6	170	2 Q925S2	Q925s2 mus musculu
11	514.5	40.3	470	2 Q7TMM1	Q7tmk1 mus musculu
12	502.5	39.4	472	2 Q6PUA7	Q6puj7 mus musculu
13	496	38.9	112	2 Q8K1F0	Q8k1f0 mus musculu
14	495.5	38.8	488	2 Q91WR1	Q91wr1 mus musculu
15	492.5	38.6	118	1 HV51 MOUSE	P06330 mus musculu
16	491	38.5	107	1 KV6F MOUSE	P04940 mus musculu
17	486	38.1	107	1 KV6I MOUSE	P04943 mus musculu
18	486	38.1	117	2 Q9QXE9	Q9qxe9 mus musculu
19	485	38.0	107	1 KV6H MOUSE	P04942 mus musculu
20	485	38.0	120	2 Q920E8	P020e8 mus musculu
21	484	37.9	107	1 KV6G MOUSE	P04941 mus musculu
22	483	37.9	117	2 Q9QXF0	Q9qxf0 mus musculu
23	482	37.8	134	2 Q8VDD0	Q8vdd0 mus musculu
24	481.5	37.7	481	2 Q8VCV5	Q8vcv5 mus musculu
25	480	37.6	107	1 KV6J MOUSE	P04944 mus musculu
26	478	37.5	117	1 HV12 MOUSE	P01756 mus musculu
27	478	37.5	117	1 HV13 MOUSE	P01757 mus musculu
28	473	37.1	134	2 Q65ZR6	Q65zr6 mus musculu
29	472.5	37.0	473	2 Q9D8L4	Q9d8l4 mus musculu
30	468	36.7	112	2 Q8K1F2	Q8k1f2 mus musculu
31	467	36.6	465	2 Q6PUB2	Q6pjb2 mus musculu

32	466	36.5	123	2 Q8VIJ1	Q8vij1 mus musculu
33	462	36.2	136	1 HV15 MOUSE	P01759 mus musculu
34	459	36.0	481	2 Q91WT1	Q91wt1 mus musculu
35	457	35.8	112	2 Q8K1F3	Q8k1f3 mus musculu
36	457	35.8	114	2 Q8K1F1	Q8k1f1 mus musculu
37	453.5	35.5	482	2 Q8K172	Q8k172 mus musculu
38	453	35.5	142	2 Q925S3	Q925s3 mus musculu
39	451	35.3	147	2 Q925S3	Q925s3 mus musculu
40	450.5	35.3	145	2 Q924R3	Q924r3 mus musculu
41	447.5	35.1	139	1 HV07 MOUSE	P01751 mus musculu
42	447.5	35.1	145	2 Q924Q7	Q924q7 mus musculu
43	447.5	35.1	145	2 Q924R1	Q924r1 mus musculu
44	445	34.9	120	1 HV03 MOUSE	P01747 mus musculu
45	445	34.9	480	2 Q8K0Z4	Q8k0z4 mus musculu

ALIGNMENTS

RESULT 1

ID	Q7TQM2	PRELIMINARY;	PRT;	243 AA.
AC	Q7TQM2;			
DT	01-OCT-2003 (Tremblrel. 25, Created)			
DT	01-OCT-2003 (Tremblrel. 25, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	ScFv 6H8 protein (Fragment).			
GN	Name=ScFv 6H8;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Balb/C;			
RX	MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;			
RA	Peter J.C., Eftekhari P., Billiaid P., Wallukat G., Hoebeke J.;			
RT	"scfv single chain antibody variable fragment as inverse agonist for			
RT	the beta-2 adrenergic receptor."			
RL	J. Biol. Chem. 278:36740-36747(2003).			
DR	EMBL; AJ574851; CAB00495.1; -.			
DR	HSSP; P01751; 1A6W.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	SMART; SM00406; IGV; 2.			
DR	PROSITE; PSS0835; IG_LIKE; 2.			
FT	NON_TER			
SO	SEQUENCE	243 AA; 25976 MW; BEFFF64D2DCFAF76 CRC64;		

Query Match 62.1%; Score 792.5; DB 2; Length 243;
Best Local Similarity 64.9%; Pred. No. 4.1e-51;
Matches 157; Conservative 30; Mismatches 48; Indels 7; Gaps 4;

QY	2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 61
Db	1 QVQLQSGSELVRPGASVKLSCKASGYTFTTYWMHWKQRHGGLEWIGNIYPPSGITNY 60
QY	62 NQKFRGKATLTVDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRGFDYWGQGTITVSSG 121
Db	61 DEKFKNGKILVTDTSSSTAYMHLSLASEDSAVYYCARG---GRGLDVWGAGTLLTVSSG 117
QY	122 VGGSGGGSGGGSDIELTQSPAIMSASPGKVTMTCSASSV-SYMHWYQKSGTSPKR 180
Db	118 GGGSGGGSGGGSDIQMTQSSSSFSVSLGDRVITTCASEDLYNRLAWYQKGNAPRL 177
QY	181 WIYDTSKLASGVPRFSGSGSGNSYSLTISVEAEADATYYCOQ-WSGYPLTFGAGTKLE 239
Db	178 LISGATSLETGVSFRFSGSGSGKDYTLISLTQTEDVATYYCQQYWS--TRTFGGGTKLE 235
QY	240 IK 241
Db	236 IK 237

```
RESULT 2
Q65ZC8
ID Q65ZC8 PRELIMINARY; PRT; 244 AA.
AC Q65ZC8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13057; CAA73500.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match
Best Local Similarity 61.4%; Score 783.5; DB 2; Length 244;
Matches 149; Conservative 39; Mismatches 52; Indels 3; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 61
DB 1 QVQLVQSGAEVKKPGDSVKVSKASGYTSDHYMHWRQAPGGLEWMGWIDPNNGDTRF 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARGGYDGR--GFDYWGQGTITVYS 119
DB 61 AQRPGRYTMTTRDTISAAVMEVSRRLRSDTAVYYCARREGTSAIYGMVWGQGTITVYS 120
QY 120 SGVGGSGGGSGGGSDIELTQSPAIMSASPGKVTMTCSASSSV-SYMHWYQKSGTSP 178
DB 121 SGGGGSGGGSGGGSDIQMTQSPSTLSASIGDRVTTTCRASEGITYHMLAWYQKPGKAP 180
QY 179 KRWIYDTSKLASGVPRFSGSGSGNSYSLTISVEAEDATYYCQQWSGYPLTFGAGTKL 238
DB 181 KFLIYKASSLASGAPSRFSGSGSGTDFTLTISLQPPDPAFYCCQYISNYPLTFGGGTYL 240
QY 239 EIK 241
DB 241 EIK 243

RESULT 3
Q65ZL2
ID Q65ZL2 PRELIMINARY; PRT; 487 AA.
AC Q65ZL2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Fv/M4.
GN Name=M4-IFN-<tau>;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96272580; PubMed=8688499;
```

```
RA Qi Y., Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
RT antibody secreted from myeloma cells.";
RL Hum. Antibodies Hybridomas 6:161-166(1995).
DR EMBL; S82493; AAB37424.2; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 487 AA; 53578 MW; C7EAB69F30555504 CRC64;

Query Match
Best Local Similarity 60.5%; Score 771.5; DB 2; Length 487;
Matches 153; Conservative 28; Mismatches 53; Indels 7; Gaps 3;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 61
DB 20 QVQLVQSGDAELVKPGASVKISCKASGYTFTDHAIHAKQKPEGLIEWIGISPDNDIKY 79
QY 62 NQKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARGGYDGRGFDYWGQGTITVSSG 121
DB 80 NEKFRGKATLTADKSSSTAYMDLNSLTSEDSAVYFCRSTY-----GHWGQGTITLT-GSG 133
QY 122 VGGSGGGSGGGSDIELTQSPAIMSASPGKVTMTCSASSSV-SYMHWYQKSGTSPKR 180
DB 134 GGGSGGGSGGGSGSRIQMTQSPASLSVSGELVTTTCRASENITSNLAWYQKQKSPQL 193
QY 181 WIYDTSKLASGVPRFSGSGSGNSYSLTISVEAEDATYYCQQWSGYPLTFGAGTKLEI 240
DB 194 LVYAATNLADGVPRFSGSGSGTGYSLKINSIQSEDFGSYYCQHFWGTPYTFGGGTRLEI 253
QY 241 K 241
DB 254 K 254

RESULT 4
Q6KB05
ID Q6KB05 PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ScFv B8E5 protein (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ746180; CAG34081.1; -.
DR HSSP; P01837; 1KCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
```

FT NON_TER 1 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 57.5%; Score 733.5; DB 2; Length 255;
Best Local Similarity 57.6%; Pred. No. 1e-46;
Matches 144; Conservative 35; Mismatches 60; Indels 11; Gaps 3;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
Db 1 QVQLQSGGDLVKGSLKLVSCASGFTFSSYGMWVRQTPDKRIEAWATITSGSYTY 60

QY 62 NQKFRGKATLTVDKSSSTAYMDLISLTSSEDAVYFCARG---GYDGRGFDYWGQTTVTV 118
Db 61 PDSYKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCARHINRYDG-AFDYWGQTTLTV 119

QY 119 SSGVGSGSGGSGGSDIELTQSPAIMSASPEKVTMTCSASSV-----SYHWYQ 171
Db 120 SSGGGSGGGSGGSDIVMAQSPSLVSAGEKIMSCKSQSLNSRNQXNYLAWYQ 179

QY 172 QKSGTSPKRWIYDTSKLASGVPGFRFSGSGSGNSYSLTISVVEAEDDATYCCQWMSGYPLT 231
Db 180 QKPGQSPKLLIYGASTRESGVPRFTGSGSGTDTLTISVQAEIDLAVYYCCQNDHSYPLT 239

QY 232 FGAGTKLEIK 241
Db 240 FGAGTKLEIK 249

RESULT 5

Q921A6 PRELIMINARY; PRT; 241 AA.

AC Q921A6; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; Pubmed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -.

DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; 1BMW.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
FT NON_TER 1 1
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 56.9%; Score 726.5; DB 2; Length 241;
Best Local Similarity 58.8%; Pred. No. 3.2e-46;
Matches 144; Conservative 34; Mismatches 56; Indels 11; Gaps 5;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
Db 1 QVQLQSGPELKKPGETVKISCKASGYFTFTDYGMMWVQAQPKGLKMGWINTYTGEPY 60

QY 62 NQKFRGKATLTVDKSSSTAYMDLISLTSSEDAVYFCARGGYDGRGFDYWGQTTVTVSSG 121
Db 61 ADDFKGRFAFSLFETASTAYLQINNLKNEEDTATYFCARKDL-LRYFDYWGQTTVTVSSG 119

QY 122 VGGSGGGSGGGSDIELTQSPAIMSASPEKVTMTCSASSVS-YMHWYQKSGTSPKR 180
Db 120 GGGSGGGSGGGSDIELTQSPSLASLGGKVTITCKASQDINKYIAWYQHKQKGRPS 179

QY 181 ----WIYDTSKLASGVPGFRFSGSGSGNSYSLTISVVEAEDDATYCCQWMSGYPLTFGAGT 236
Db 180 AHTLHIY----IQGIPSRFSGSGSGRDIYSFISINLEPEDIAITYCLHYDNLH-TFGGCT 234

RESULT 6

Q9QYF0 PRELIMINARY; PRT; 298 AA.

AC Q9QYF0; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CN 8 single chain antibody.
GN Name=CN 8 scFv;
OS synthetic construct.
OC other sequences; artificial sequences.
OX NCBI_TaxID=32630;

RP SEQUENCE FROM N.A.
RX MEDLINE=20183931; Pubmed=10706631; DOI=10.1073/pnas.050582197;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phage display subtraction
RT method.";
RI Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL; AB036341; BAA88633.1; -.

DR PIR; A33933; A33933.
DR PIR; S19112; S19112.
DR HSSP; P01820; 1A7O.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 56.4%; Score 720; DB 2; Length 298;
Best Local Similarity 58.1%; Pred. No. 1.2e-45;
Matches 140; Conservative 33; Mismatches 66; Indels 2; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
Db 40 QVQLQSGGGLVPGSLKLSGASGSDFSRYMWSWVRQAPGKLEWIGEINPDSSTINY 99

QY 62 NQKFRGKATLTVDKSSSTAYMDLISLTSSEDAVYFCARGGYDGRGFDYWGQTTVTVSSG 121
Db 100 TPSLKDKFIISRDNKNTLYLQMSKVRSEDTALYYCARASYGHS-AYWGQTTVTVSSG 158

QY 122 VGGSGGGSGGGSDIELTQSPAIMSASPEKVTMTCSASSV-SYHWYQKSGTSPKR 180
Db 159 GGGSGGGSGGGSDIELTQSPASLSASVGETVITTCRASGNHNYLAWYQKQKSPOL 218

QY 181 WIYDTSKLASGVPGFRFSGSGSGNSYSLTISVVEAEDDATYCCQWMSGYPLTFGAGTKLEI 240
Db 219 LVYNAKTLADGPSRFSFGSGSGTQYSLKINSIQPEDFGSYCQHFWTTPYTFGGGKLEI 278

QY 241 K 241
Db 279 K 279

RESULT 7

O65ZC9 PRELIMINARY; PRT; 240 AA.

ID O65ZC9; 25-OCT-2004 (TREMBLrel. 28, Created)

DT 25-OCT-2004 (Tremblrel. 28, last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 56.3%; Score 718.5; DB 2; Length 240;
Best Local Similarity 57.4%; Pred. No. 1.3e-45;
Matches 139; Conservative 43; Mismatches 55; Indels 5; Gaps 4;

QY 2 QVQLQQSGPELEKPGASVKLSCKASGYSTGYTMNWVKQSHGKSLIEWIGLITPYNGASS-60
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAVIS-YDGSNKY 59

QY 61 YNOKFRGKATLTVDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRGFDYWGQGTITVTVSS 120
Db 60 YADSVKGRFTISRDNKNTLYIQMNSLRPEDTAVVYCARDW--GDSLDPWGKGTLVTVSS 117

QY 121 GVGSGGGGGGGGGSDIELTQSPAIMASPGKVTMTCSASSSV-SYMHVYQOKSGTSPK 179
Db 118 GGGSGGGGGGGGGSDIQMTQSPSTLSASIGDRVITCRASEGIYRWLAWYQOKPKAPK 177

QY 180 RWIYDTSKLASGVPRFGSGSGNSYSLTISVVEAEDDATYYCCQWSGYPLTFGAGTKLE 239
Db 178 LLTYKASSLASRAPSRFGSGSGTDFTLTISLQPDPAFYCCQYSNYPLTFGGGTGLE 237

QY 240 IK 241
Db 238 IK 239

RESULT 8
Q65ZQ7 PRELIMINARY; PRT; 248 AA.
ID Q65ZQ7
AC Q65ZQ7;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, last annotation update)
DE B3 (Fv)-PE40 (Fragment).
GN Name=B3 (Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pal L.H., Fitzgerald D.J., Willingham M., Pastan I.;
RT "B3 (Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
RT regression of a human carcinoma in mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR EMBL; S57990; AAB19971.2; -.

DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
FT NON_TER 248
FT NON_TER 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 50.5%; Score 645; DB 2; Length 248;
Best Local Similarity 51.0%; Pred. No. 3.8e-40;
Matches 126; Conservative 41; Mismatches 74; Indels 6; Gaps 1;

QY 1 MQVQLQQSGPELEKPGASVKLSCKASGYSTGYTMNWVKQSHGKSLIEWIGLITPYNGASS 60
Db 1 MDVXLVESGGGLVQPGGSLKLSCATSGFTFSDYMYWVRQTPERKLEWVAVISNDSSAA 60

QY 61 YNOKFRGKATLTVDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRGFDYWGQGTITVTVSS 120
Db 61 YSDTYKGRFTISRDNARNTLYIQMSRLKSEDTAIFYSCARGLAWGAFAYWGQGTITVTVSS 120

QY 121 GVGSGGGGGGGGGSDIELTQSPAIMASPGKVTMTCSASSSV-----SYMHVYQOKS 174
Db 121 GGGSGGGGGGGGGSDVLTMTQSPFLPSLIGDQASISCRSSQILVHSGNTLYLEWYLOKP 180

QY 175 GTSPEKRWIYDTSKLASGVPRFGSGSGNSYSLTISVVEAEDDATYYCCQWSGYPLTFGA 234
Db 181 GQSPKLLIYKVSNNRFGVPPDRFGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVFTFGS 240

QY 235 GTKLEIK 241
Db 241 GTKLEIK 247

RESULT 9
Q925S1 PRELIMINARY; PRT; 218 AA.
ID Q925S1
AC Q925S1;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR HSSP; P01665; IQNZ.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 218
FT NON_TER 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 49.2%; Score 628; DB 2; Length 218;
Best Local Similarity 55.8%; Pred. No. 6e-39;

[illegible]

RESULT 10		
O925S2		
ID O925S2	PRELIMINARY;	PRT; 170 AA.
AC O925S2;		
DT 01-DEC-2001	(TREMBLrel, 19, Created)	
DT 01-DEC-2001	(TREMBLrel, 19, Last sequence update)	
DT 01-OCT-2003	(TREMBLrel, 25, Last annotation update)	
DE MRP4.		
OS Mus musculus (Mouse).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX NCBI_TaxID=10090;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN=BALB/c;		
RX PubMed=11819679;		
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,		
RA Su C.;		
RT "Mechanism of exogenous nucleic acids and their precursors improving		
RT the repair of intestinal epithelium after irradiation in mice.";		
RL World J. Gastroenterol. 6:709-717(2000).		

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Cui D., Zeng G., Yan X., Li X., Su C.;
 RT "Cloning of mouse genes related to repairing of intestinal epithelium
 RT of the irradiated mice by treatment with the intestinal RNA of mice of
 RT the same strain.";
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
 DR EMBL; AF240167; AAK43732.1; --
 DR HSSP; P01751; 1A6W.
 DR SMART; SM00406; IGV, 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 SQ SEQUENCE 170 AA; I7978 MW; 5042823CC6C10F38 CRC64;

Query Match	42.6%;	Score 543;	DB 2;	Length 170;
Best Local Similarity	66.4%;	Pred. No. 9.4e-33;		
Matches 101; Conservative	23;	Mismatches 16;	Indels 12;	Gaps 2;
QY	2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGTMMNWVKOSHGSLEWIGLITPYNGASSY	61		
Dd	3 QVRLQQSGPEVVRPGVSVKISCKSGSYFTFDYSMHWLKNHAKSLSEWIGLISITYDGNTRY	62		
QY	62 NQKFRGKATLTVDKSSSTAYMDLLTSEDSAVFECARGGYDR--GFDPWGCGTTVTVS	119		
Dd	63 NQKFEGKATMTVDKSSITAYMEARLTSDSALTYCARGAAYGSSFYFDYWGGTTVTVS	122		
QY	120 SGVGSGGGGGSGGGSDIELTQSPAIMSAPG	151		
Dd	123 SGGGGSGGGGGSGGSGE-----SSSPG	144		

RESULT 11
Q7TMK1

ID	Q7TMK1	PRELIMINARY;	PRT;	470 AA..
----	--------	--------------	------	----------

DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hypotheetical protein A1324046.
 GN Name=A1324046;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI TaxID=10090;

[1]
RN SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Plante S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences ";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055910; AAH55910.1; -.
DR HSP; P01865; 1KB5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51727 MW; 6D90E4DFB96BB090 CRC64;

Query Match	40.3%	Score 514.5;	DB 2;	Length 470;
Best Local Similarity	52.1%;	Pred. No. 3:8e-30;		
Matches 122;	Conservative 19;	Mismatches 46;	Indels 47;	Gaps 8;

```
QY      2 QVQLQQSGPELEKPKASVKLSCKASGYSFTGTMTNMWVKQSHKSLIEWIGLTPYNGASSY 61
      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db      20 EVQLQQSGPELVKPKASVKISCKASGYTFTGYTHMWVKQSHGSLIEWIGLVNPSNGDTSY 79

QY      62 NQKFRKATLTVDKSSSTAYMDLISLTSEDSAVYECARGGYDGR--GFDYWGQCTTVTVS 119
      ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db      80 NQKFKGKATLTVDKSSSTAYMEINSLTSEDSAVYYCARYYVYSGSYWYFDWVGAGTTTVTS 139

QY      120 SGVGGGGGGGGGGSDIELTQSPAIMSASP-----GEKYTMTCSSASSSVYMHMYQOK 173
      | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db      140 SAT-----TTAPSVYPLVPGCGDTSGSVTLGCLV----- 169
```

```
QY      174 SGTSPK---RWIYDTSKLASGVPRFGSGSGNSYSYLTISSVEAEDDATYYCQ   223
          | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db      170 KGYPPEPVTVKKMY--GALSSGVRTVSSLQSG-FYSL--SSLVTVPSSSTWPSQ  218
```

```
RESULT 12
Q6PJA7
ID Q6PJA7 PRELIMINARY; PRT; 472 AA.
AC Q6PJA7;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Strapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hejton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018535; AAH18535.1; -.
DR HSSP; P01865; 1KB5.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Ig_c1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 52299 MW; 165169C23D55D4AB CRC64;

Query Match 39.4%; Score 502.5; DB 2; Length 472;
Best Local Similarity 46.1%; Pred. No. 3e-29;
Matches 118; Conservative 26; Mismatches 59; Indels 53; Gaps 9;
```

```
QY 171 QOKSGTSPKRWIYDTSKLASGVGRFSGSGSGNSYSTLTSSVEAEDDATYCCQWGSYPL 230
DB 176 -----PEPVTLTWNSGSLSSGV-HTFPAVLQSDLYTLSSS-----VTVTSSTWPSQSI 222
QY 231 TF-----GAGTKLEIK 241
DB 223 TCNVAHPASSTKVDKK 238

RESULT 13
Q8K1F0
ID Q8K1F0 PRELIMINARY; PRT; 112 AA.
AC Q8K1F0;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516285; AAM64203.1; -.
DR PIR; A33933; A33933.
DR PIR; PC4405; PC4405.
DR HSSP; P01837; 1ORQ.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
FT NON_TER 112
SQ SEQUENCE 112 AA; 11901 MW; F6644663201AA239 CRC64;

Query Match 38.9%; Score 496; DB 2; Length 112;
Best Local Similarity 92.2%; Pred. No. 1.8e-29;
Matches 95; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 139 LTQSPAIMSASPEKVTMTCSASSSVSYMHYQOKSGTSPKRWIYDTSKLASGVGRFSG 198
DB 4 LTQSPAIMSASPEKVTMTCSASSSVSYMHYQOKSGTSPKRWIYDTSKLASGVGRFSG 63
QY 199 SSGNSYSTLTSSVEAEDDATYCCQWGSYPLTFGAGTKLEIK 241
DB 64 SSGNSYSTLTSSVEAEDDATYCCQWGSNPNPTFGGKTLEIK 106

RESULT 14
Q91WR1
ID Q91WR1 PRELIMINARY; PRT; 488 AA.
AC Q91WR1;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 24, 2005, 18:46:59 ; Search time 42 Seconds
(without alignments)
428.343 Million cell updates/sec

Title: US-09-979-539-1

Perfect score: 1276

Sequence: 1 MQVQLQSGPELEKPGASVK.....CQQWSGYPLTFGAGTKLEIK 241

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	1274	99.8	241	US-09-581-345-5	Sequence 5, Appli
2	993	77.8	244	US-08-553-497A-20	Sequence 20, Appl
3	987	77.4	242	US-08-553-497A-26	Sequence 26, Appl
4	982.5	77.0	297	US-09-486-814A-2	Sequence 2, Appli
5	981.5	76.9	599	US-08-463-163-3	Sequence 3, Appli
6	979	76.7	244	US-08-553-497A-22	Sequence 22, Appl
7	977	76.6	242	US-08-553-497A-28	Sequence 28, Appl
8	976.5	76.5	239	US-08-279-772A-8	Sequence 8, Appli
9	976.5	76.5	239	US-08-902-486-11	Sequence 11, Appl
10	972	76.2	246	US-08-553-497A-24	Sequence 24, Appl
11	959.5	75.2	256	US-09-526-738A-2	Sequence 2, Appli
12	959.5	75.2	258	US-09-526-738A-4	Sequence 4, Appli
13	956.5	75.0	495	US-09-948-004-18	Sequence 18, Appl
14	908	71.2	238	US-09-798-689-21	Sequence 21, Appl
15	902.5	70.7	246	US-08-469-486-57	Sequence 57, Appl
16	902.5	70.7	246	US-08-469-486-57	Sequence 57, Appl
17	889.5	69.7	270	US-08-652-507-2	Sequence 2, Appli
18	885.5	69.4	281	US-09-423-439-44	Sequence 44, Appl
19	885.5	69.4	666	US-09-423-439-51	Sequence 51, Appl
20	883.5	69.2	553	US-08-661-052-16	Sequence 16, Appl
21	883.5	69.2	553	US-09-188-082-16	Sequence 16, Appl
22	883.5	69.2	553	US-09-364-088-16	Sequence 16, Appl
23	883.5	69.2	553	US-09-102-716-16	Sequence 16, Appl
24	866	67.9	267	US-09-485-737B-2	Sequence 2, Appli
25	866	67.9	267	US-10-071-485-2	Sequence 2, Appli
26	866	67.9	541	US-09-485-737B-85	Sequence 85, Appl
27	866	67.9	541	US-10-071-485-85	Sequence 85, Appl

28	866	67.9	711	3	US-09-485-737B-90	Sequence 90, Appl
29	866	67.9	711	4	US-10-071-485-90	Sequence 90, Appl
30	854	66.9	284	3	US-09-184-658-40	Sequence 40, Appl
31	854	66.9	284	4	US-09-504-262D-40	Sequence 40, Appl
32	849.5	66.6	255	3	US-09-553-498-8	Sequence 8, Appli
33	849.5	66.6	255	4	US-09-618-869-8	Sequence 8, Appli
34	841.5	65.9	273	2	US-08-403-853-18	Sequence 18, Appl
35	841	65.9	235	2	US-08-190-199A-61	Sequence 61, Appl
36	839	65.8	267	4	US-09-419-788-30	Sequence 30, Appl
37	834.5	65.4	240	3	US-09-485-737B-91	Sequence 91, Appl
38	834.5	65.4	240	4	US-10-071-485-91	Sequence 91, Appl
39	831.5	65.2	240	2	US-08-800-198-8	Sequence 8, Appli
40	831.5	65.2	240	3	US-09-296-595-8	Sequence 38, Appl
41	829	65.0	288	3	US-09-423-439-38	Sequence 32, Appli
42	829	65.0	673	3	US-09-423-439-32	Sequence 32, Appli
43	823	64.5	260	2	US-08-447-402-1	Sequence 1, Appli
44	822.5	64.5	236	2	US-08-190-199A-65	Sequence 65, Appl
45	822	64.4	249	2	US-08-797-689-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-581-345-5
; Sequence 5, Application US/09581345
; Patent No. 6809184
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Chowdhury, Partha S.
; APPLICANT: The Government of the United States
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Antibodies, including Fv Molecules, and
; TITLE OF INVENTION: Immunocjugates Having High Binding Affinity for
; FILE REFERENCE: 015280-339100US
; CURRENT APPLICATION NUMBER: US/09/581,345
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/067,175
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: WO PCT/US98/25270
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SS scFv
US-09-581-345-5

Query Match 99.8%; Score 1274; DB 4; Length 241;
Best Local Similarity 99.6%; Pred. No. 2.4e-95;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MQVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLWIGLITPYNGASS	60
DB	1	MQVQLQSGPELEKPGASVKISCKASGYSFTGYTMNWVKQSHGKSLWIGLITPYNGASS	60
QY	61	YNQKFRGKATLTVDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRGFDYWGQGTIVTSS	120
DB	61	YNQKFRGKATLTVDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRGFDYWGQGTIVTSS	120
QY	121	GVGSGGGGSGGGSDIELTQSPAIMASPGKVTMTCSASSSVSYMHWYQKSGTSPKR	180
DB	121	GVGSGGGGSGGGSDIELTQSPAIMASPGKVTMTCSASSSVSYMHWYQKSGTSPKR	180
QY	181	WIYDTSKLASGVGRFRSGSGNSYSLTISVVEAEDDATYYCQQWSGYPLTFGAGTKLEI	240
DB	181	WIYDTSKLASGVGRFRSGSGNSYSLTISVVEAEDDATYYCQQWSGYPLTFGAGTKLEI	240

Matches 192; Conservative 16; Mismatches 32; Indels 2; Gaps 1;

QY 2 QVQLQSGPELEKPGASVSKLSCKASGYSFTGYTMNWVKOSHGKSLIEWIGLITPYNGASSY 61
 Db 1 QVKLOESGAELVKGASVSKLSCKASGYSFTSHMMHWKORAGQGLEWIGELINPRTAPNTY 60

QY 62 NQKRRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARG--GYDGRGPDYWGQGTIVTVS 119
 Db 61 NEKFRSKATLTVDKSSSTAYMDLSTLSEDSAVYFCASRDYDGRYFDYWGQGTIVTVS 120

QY 120 SGVSGSGSGSGSGSDIELTQSPAIMSAPGEKVTMTCSASSSVSTMHWYQOKSGTSPK 179
 Db 121 SGGSGSGSGSGSGSDIELTQSPITMSASPGKVTMTCSASSSVSTYTWYQOKTSSPR 180

QY 180 RWIYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYCCQWNGYPLTFGAGTKLE 239
 Db 181 LLIVTSLNLASGVPRFSGSGSGTSLTISRMEADDAATYCCQWSSYPLTFGAGTKLE 240

QY 240 IK 241
 Db 241 IK 242

RESULT 4

US-09-486-814A-2
 ; Sequence 2, Application US/09486814A
 ; Patent No. 6562599
 ; GENERAL INFORMATION:
 ; APPLICANT: YAMAMOTO, Masato
 ; APPLICANT: HAYASHI, No. 6562599io
 ; APPLICANT: YAMAMOTO, Hiroko
 ; APPLICANT: TOHDOH, Naoki
 ; TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
 ; TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
 ; FILE REFERENCE: 0020-4682P
 ; CURRENT APPLICATION NUMBER: US/09/486, 814A
 ; CURRENT FILING DATE: 2002-06-13
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 297
 ; TYPE: PRT
 ; ORGANISM: Mus sp., strain: Balb/c, tissue: spleen
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)..(145)
 ; OTHER INFORMATION: Identification Method: P
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (177)..(279)
 ; OTHER INFORMATION: Identification Method: P
 US-09-486-814A-2

Query Match 77.0%; Score 982.5; DB 4; Length 297;
 Best Local Similarity 78.7%; Pred. No. 1e-71;
 Matches 192; Conservative 15; Mismatches 28; Indels 9; Gaps 3;

QY 2 QVQLQSGPELEKPGASVSKLSCKASGYSFTGYTMNWVKOSHGKSLIEWIGLITPYNGASSY 61
 Db 40 QVKLOESGPELEKPGASVSKLSCKASGYSFTGYTMKWVQKSLIEWIGIITYPYNGGTGY 99

QY 62 NQKFRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGGYDGRGFDYWGQGTIVTVSSG 121
 Db 100 NQKFRKATLTVDKSSSTAYMDLSTLSEDSAVYFCAR----LGLDYWGQGTIVTVSSG 154

QY 122 VGGSGSGSGSGSGSDIELTQSPAIMSAPGEKVTMTCSASSSV--YHMYQOKSGTSPK 179
 Db 155 GGGSGSGSGSGSGSDIELTQSPITMAASGEKITITCSASSSISNLYHMYQOKPGFSPK 214

QY 180 RWIYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYCCQWNGYPLTFGAGTK 237
 Db 215 LLIVTSLNLASGIPARFSGSGTSLTIGTMEADDAATYCCQWSSYPLTFGAGTK 274

QY 238 LEIK 241
 Db 275 LEIK 278

RESULT 5

US-08-463-163-3
 ; Sequence 3, Application US/08463163
 ; Patent No. 5696237
 ; GENERAL INFORMATION:
 ; APPLICANT: Fitzgerald, David J.
 ; APPLICANT: Chaudhary, Vijay K.
 ; APPLICANT: Pastan, Ira H.
 ; APPLICANT: Waldmann, Thomas A.
 ; APPLICANT: Queen, Cary L.
 ; TITLE OF INVENTION: Recombinant Antibody-Toxin Fusion Protein
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew
 ; STREET: One Market Plaza, Stewart Street Tower
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105-1492
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/463,163
 ; FILING DATE: 05-JUN-1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 06/227,227
 ; FILING DATE: 22-JAN-1981
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 06/911,227
 ; FILING DATE: 24-SEP-1986
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/341,361
 ; FILING DATE: 21-APR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/865,722
 ; FILING DATE: 08-APR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weber, Ellen L.
 ; REGISTRATION NUMBER: 32,762
 ; REFERENCE/DOCKET NUMBER: 015280-12211
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 543-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 599 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-463-163-3

Query Match 76.9%; Score 981.5; DB 1; Length 599;
 Best Local Similarity 78.8%; Pred. No. 2.8e-71;
 Matches 190; Conservative 14; Mismatches 34; Indels 3; Gaps 1;

QY 1 MOVQLQSGPELEKPGASVSKLSCKASGYSFTGYTMNWVKOSHGKSLIEWIGLITPYNGASS 60
 Db 1 MOVQLQSGAELAKPGASVKMSCKASGYTFTSYRMHWKORPGQGLEWIGINPSTGYTE 60

QY 61 YNOKFRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGGYDGRGFDYWGQGTIVTVSS 120
 Db 61 YNOKFRKATLTVDKSSSTAYMDLSTLSEDSAVYFCAR--GGVFDYWGQGTIVTVSS 117

```

QY      121 GVGSGSGGGSGGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYMHVYQOKSGTSPKR 180
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      118 GGGGSGGGSGGGGSGQIVLTQSPAIMSASPEKVTITCSASSISYMHWFQOKPGTSPKL 177
QY      181 WIYDTSKLASGVPRFSGSGSGNSYSLTISSEAEADATYVYQQQWSGVPPLFGAGTKLEI 240
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      178 WIYTTSNLASGVPARFSGSGSGTYSYLTISRMEAEADATYVYCHQRSTYPLTFGSGTKLEL 237
QY      241 K 241
      |
Db      238 K 238

```

```

RESULT 6
US-08-553-497A-22
; Sequence 22, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLEBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANCESCA
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PIULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-553-497A-22

Query Match 76.7%; Score 979; DB 2; Length 244;
Best Local Similarity 78.7%; Pred. No. 1.5e-71;
Matches 192; Conservative 15; Mismatches 33; Indels 4; Gaps 2;

```

[illegible]

```

RESULT 7
US-08-553-497A-28
; Sequence 28, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLEBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANCESCA
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PILATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:

```

LENGTH: 242 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-28

Query Match 76.6%; Score 977; DB 2; Length 242;
Best Local Similarity 78.1%; Pred. No. 2.2e-71;
Matches 189; Conservative 19; Mismatches 32; Indels 2; Gaps 1;

QY 2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
Db 1 EVKLQQSGAELVKGASVKLSCKASGYFTSHLDHWKQRGWQGLEWIGQFNPSNGRTNY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDAVYFCARG--GYDGRGFDYWGQGTITVVS 119
Db 61 NEKFKSKATLTVDKSSSTAYIELSLTSEDCSVYCCASRDYDGRYFDYWGQGTITVVS 120
QY 120 SGVGGSGGSGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHVYQKSGTSPK 179
Db 121 SGGGGSGGSGGSDIELTQSPTIMSASPGKVTMTCSASSSVSYMYWYQKGTSSPR 180
QY 180 RWIYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYYCQWMSGYPLTFGAGTKLE 239
Db 181 LLTYDTSNLASGVPRFSGSGSGTISLTISRMEADATYYCQWSSYPLTFGAGTKLE 240
QY 240 IK 241
Db 241 IK 242

RESULT 8
US-08-279-772A-8
Sequence 8, Application US/08279772A
Patent No. 6080560

GENERAL INFORMATION:
APPLICANT: Russell, David R
APPLICANT: Fuller, James T
TITLE OF INVENTION: Method for Producing Antibodies in Plant
TITLE OF INVENTION: Cells
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
STREET: PO Box 2113
CITY: Madison
STATE: WI
COUNTRY: United States of America
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,772A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-279-772A-8

Query Match 76.5%; Score 976.5; DB 3; Length 239;

Best Local Similarity 78.8%; Pred. No. 2.4e-71;
Matches 189; Conservative 14; Mismatches 34; Indels 3; Gaps 1;

QY 2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
Db 3 QVQLQQSGAELAKPGASVKMSCKASGYFTSYRMHWKQRPQGLEWIGYINPSTGYTEY 62
QY 62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDAVYFCARGGYDGRGFDYWGQGTITVSSG 121
Db 63 NQKFKDKATLTADKSSSTAYMDLSLTFEDSAVYYCARG--GVFDYWGQGTITLVSSG 119
QY 122 VGGSGGGSGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHVYQKSGTSPKRW 181
Db 120 GGGSGGGSGGSGQIVLTQSPAIMSASPGKVTITCSASSISYMHVFOQKPGTSPKLW 179
QY 182 TYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYYCQWMSGYPLTFGAGTKLEIK 241
Db 180 IYTTSNLASGVPRFSGSGSGTISLTISRMEADATYYCHQRSTYPLTFGSGTKLELK 239

RESULT 9
US-08-902-486-11
Sequence 11, Application US/08902486
Patent No. 6140075

GENERAL INFORMATION:
APPLICANT: Russell, David R.
APPLICANT: Fuller, James T.
TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND
TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,486
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 670513.90261
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-902-486-11

Query Match 76.5%; Score 976.5; DB 3; Length 239;
Best Local Similarity 78.8%; Pred. No. 2.4e-71;
Matches 189; Conservative 14; Mismatches 34; Indels 3; Gaps 1;

QY 2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
Db 3 QVQLQQSGAELAKPGASVKMSCKASGYFTSYRMHWKQRPQGLEWIGYINPSTGYTEY 62
QY 62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDAVYFCARGGYDGRGFDYWGQGTITVSSG 121
Db 63 NQKFKDKATLTADKSSSTAYMDLSLTFEDSAVYYCARG--GVFDYWGQGTITLVSSG 119


```

; NUMBER OF SEQ ID NOS
; SOFTWARE: PatentIn
; SEQ ID NO 4
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Humanus
US-09-526-738A-4

```

Query Match	75.2%;	Score 959.5;	DB 4;	Length 258;
Best Local Similarity	77.6%;	Pred. No. 6.2e-70;		
Matches 187;	Conservative 13;	Mismatches 36;	Indels 5;	Gaps 2;

```

Oy      2  OVOLOQSGPELEKPGASVKLSCKASGYSFTGYTMNWNVKQSHGSKLEWIGLITPYNGASSY 61
      ||:||||| || |||||:||||:||||| ||:||||| ||:|
Db      3  OVKLQSGAEILAKPGASVKMSCTGTYFTFTSYMNWNVKORPGGLEWIGYINPTGYTKY 62

```

```
QY      62 NQKFRGKATLTVDKSSSTAYMDLLSTSEDSAVYFCARG-GYDGRGPDYWGQGTIVTSS 120
      |||:||||| ||||| |||:|||||:| ||||| ||||| |||||
Db      63 NQKFRKATLTADKSSSTAYMOLLSLTNVDSAVYCTTGYSY---FDYWGQGTIVTSS 118
```

```
Oy      121 GVGSGGGGSGGGSDIELTQSPAIMSASPEKVTMTCSASSVSVMHWYQQKGSTSPKR 180
        | ||||| ||||| ||||| : ||||| : ||| : || |||| 
Db      119 GGGGSGGGGSGGGSDIELTQSPAIMSASPEKVITITCSASSSVNMMWFQQKPSTPKL 178
```

```
OY      181 WIYDTSKLASGVPGRFSGSGSNGNSYSLTISSEAEADATYYCQOMSGYPITFGAGTKLET   240
        |||||
Db       179 WISSTSNLASGVPARFEGSSGSTSYSLTISRMEADATYYCCOORSSYPYTFGGGTKLOT   238
```

Qy	241 K 241
Db	239 K 239

RESULT 13
US-09-948-004-18

```

; Sequence 1, Application 00/00000000
; Patent No. 6723538
; GENERAL INFORMATION:
; APPLICANT: MACK, Mathias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; TITLE OF INVENTION: immunological disorders
; FILE REFERENCE: E 2411 BP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-948-004-18

```

Query Match 75.0%; Score 956.5; DB 4; Length 495;
Best Local Similarity 76.9%; Pred. No. 2.4e-69;
Matches 186; Conservative 17; Mismatches 36; Indels 3; Gaps 1;

```

QY      3  VOLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLWIGLITPYNGASSYN 62
      :::||||| :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      248 IKIQSGAELARPGLASVKMSCTSGYTFTRLYTMHWKORPGGSEWIGYINPSRGTYNN 30

```

```
QY      63 QKFRGKATLTVDKSSSTAYMDLLSTSEDSAVYFCARGYDGRGFDYMGQTTVTVSS-- 120
      |||: ||||| ||||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
Db    308 QKFKKATLTTDKSSSTAYMQLSSLTSEDSAVYICARYDDHCLDYKROGTTLTVSSYE 367
```

Qy 121 -GVGGSGGCGSGGGSDIELTOSPAINSASPGEKVTMTCSASSSVSYNHWYQQKSCTSPK 179
| | | | | : | | | | | | | | | | | | | | | | | | | | |
Db 368 GGS GGSGSGSGSGGVDDIQLTOSPAINSASPGEKVMTCRASSSVSYNMWYQQKSCTSPK 427

```
Qy . 180 RWIYDTSKLASGVPRFSGSGSGNSYSLTISSEAEADATYYCQQWMSGYPLTFGAGTKLE 239
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 428 RWIYDTSKVASGVPRFSGSGSGTYSLTISSEAEADATYYCQQWSSNPLTFGAGTKLE 487
```

QY 240 IK 241

Db 488 LK 489

RESULT 14
US-09-798-689-21
! Sequence 21, Application US/09798689

```

; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; TITLE OF INVENTION: Combined With Radiation and Chemotherapy
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; Patent No. 6811779

```

: CURRENT FILING DATE: 2001-03-02
 : PRIOR APPLICATION NUMBER: 09/401,163
 : PRIOR FILING DATE: 1999-09-22

PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 08/706,804
PRIOR FILING DATE: 1996-09-03

PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/326,552
PRIOR FILING DATE: 1994-10-20

; PRIOR FILING DATE: 1994-02-
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.1

```

; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse

```

Query Match	71.2%;	Score 908;	DB 4;	Length 238;
Best Local Similarity	74.0%;	Pred. No. 8.1e-66;		
Matches 179; Conservative	17;	Mismatches 40;	Indels 6;	Gaps 2;

Qy 2 QVQLQSGPELEKPGASVKISCKASGYSTGYTMNWVKSHGKSLIEWIGLTIPYNGASSY 61
||:||||| || ||||| ||: ||: ||||| : ||||| || ||| ||
Db 1 QVQLQSGAEIVGSGASVKISCTTSGFNKDFYMHMWKRPQGLEWIGWIDPENGSDSY 60

```

QY      62 NQKFRGKATLTVDKSSSTAYMDLISLTSEDSAVVFCAR--GGYDGRGFYWGQTTVTVS 119
      ||:||||:| ||:||||:| ||||||:||||:| ||:| |||||||||||
Db      61 APRHOGKATMTADSSNTAYLTQLSLTSEDTAVYYCNAYYGDYEG----YWGQGTITVS 116

```

Qy 120 SGVGGSGGGSGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQOKSGTSPK 179
|||:|||||:|||||
Db 117 SGGGSGSGGGSGGGSDIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQOKPGTSPK 176

```
Qy      180 RWIYDTSKLASGVPGRFSGSGSNGSYSLTISSEVEADDATYYCQOMSGVPLTFAGATKLE 239
        ||| ||||| ||||| ||||| :||| ||||| ||| |||:||||
Db      177 LWIYSTSNLASGVPARFSGSGSGSYSLTISRMEADDATYYCQOQSSYPFTFGSGTKLE 236
```

Qy	240 IK 241
Db	237 IK 238

RESULT 15
US-08-469-486-57

```

;
; APPLICANT: Thoegersen, Hans Christian
;
; APPLICANT: Holtel, Thor Las
;
; APPLICANT: Etzerodt, Michael
;
; TITLE OF INVENTION: Improved method for the refolding of
;
; TITLE OF INVENTION: proteins
;
; NUMBER OF SEQUENCES: 58
;

```

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
. COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-486-57

Query Match 70.7%; Score 902.5; DB 1; Length 246;
Best Local Similarity 73.9%; Pred. No. 2.3e-65;
Matches 178; Conservative 15; Mismatches 37; Indels 11; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
Db 1 QVQLQSGAELVKPGASVKMSCKASGYTFASYWINWVKQRPQGLEWIGHIYPVRSITKY 60
QY 62 NQKPRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARG-GYDGRGFDYWGQGTIVTVSS 120
Db 61 NEKFRSKATLTLDTSSTAYMQLSLTSEDSAVYCSRGDSDYVAMDYWGQGTIVTVS- 119
QY 121 GVGSGGGGGSGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHWYQOKSGTSPKR 180
Db 120 -----SGGGSDIELTQSPALISASPGKVTMTCRASSSVSYMHWYQOKPGSSPKP 170
QY 181 WIYDTSKLASGVPRFSGSGSGNSYSILTISVEAEDDATYCCQWGSYPLTFGAGTKLEI 240
Db 171 WIYATSNLASGVPRFSGTSGTSTSYSLTISRVEAEDDATYCCQWSRNPFTFGSGTKLEI 230
QY 241 K 241
Db 231 K 231

Search completed: October 24, 2005, 20:07:21
Job time : 44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 24, 2005, 20:05:55 ; Search time 165 Seconds
(without alignments)
609.812 Million cell updates/sec

Title: US-09-979-539-1

Perfect score: 1276

Sequence: 1 MQVQLQSGPELEKPGASVK.....CQWMSGYPLTFGAGTKLEIK 241

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1862986 seqs, 417506248 residues

Total number of hits satisfying chosen parameters: 1862986

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1274	99.8	241	18 US-10-973-718-5	Sequence 5, Appli
2	1025.5	80.4	242	14 US-10-259-087A-20	Sequence 20, Appl
3	1025.5	80.4	242	16 US-10-689-006-20	Sequence 20, Appl
4	1010.5	79.2	239	9 US-09-808-037-6	Sequence 6, Appli
5	1010.5	79.2	239	14 US-10-162-889-6	Sequence 6, Appli
6	1010.5	79.2	239	15 US-10-384-788-6	Sequence 6, Appli
7	1010.5	79.2	239	15 US-10-618-856-6	Sequence 6, Appli
8	1010.5	79.2	239	17 US-10-749-522-6	Sequence 6, Appli
9	1010.5	79.2	239	20 US-11-073-526-6	Sequence 6, Appli
10	1003	78.6	261	16 US-10-689-006-24	Sequence 24, Appl
11	989.5	77.5	242	14 US-10-259-087A-18	Sequence 18, Appl

12	989.5	77.5	242	16	US-10-689-006-18	Sequence 18, Appl
13	967.5	75.8	492	16	US-10-682-845-63	Sequence 63, Appl
14	967.5	75.8	492	16	US-10-682-845-79	Sequence 79, Appl
15	967.5	75.8	492	16	US-10-682-845-83	Sequence 83, Appl
16	966.5	75.7	492	16	US-10-682-845-87	Sequence 87, Appl
17	966	75.7	246	17	US-10-682-845-15	Sequence 15, Appl
18	965.5	75.7	492	16	US-10-682-845-61	Sequence 61, Appl
19	965.5	75.7	492	16	US-10-682-845-71	Sequence 71, Appl
20	965.5	75.7	492	16	US-10-682-845-73	Sequence 73, Appl
21	965.5	75.7	492	16	US-10-682-845-77	Sequence 77, Appl
22	964.5	75.6	243	18	US-10-966-406-2	Sequence 2, Appli
23	964.5	75.6	409	15	US-10-362-591-2	Sequence 2, Appli
24	964.5	75.6	492	16	US-10-682-845-59	Sequence 59, Appl
25	964.5	75.6	492	16	US-10-682-845-67	Sequence 67, Appl
26	964.5	75.6	492	16	US-10-682-845-69	Sequence 69, Appl
27	964.5	75.6	499	17	US-10-805-177-111	Sequence 111, App
28	964.5	75.6	500	14	US-10-168-809-22	Sequence 22, Appl
29	963.5	75.5	492	16	US-10-682-845-75	Sequence 75, Appl
30	963.5	75.5	492	16	US-10-682-845-85	Sequence 85, Appl
31	962.5	75.4	260	15	US-10-435-614-20	Sequence 20, Appl
32	961	75.3	246	17	US-10-861-617-17	Sequence 17, Appl
33	961	75.3	657	16	US-10-723-003-48	Sequence 48, Appl
34	960.5	75.3	492	16	US-10-682-845-65	Sequence 65, Appl
35	959.5	75.2	256	14	US-10-247-488-2	Sequence 2, Appli
36	959.5	75.2	258	14	US-10-247-488-4	Sequence 4, Appli
37	957.5	75.0	492	16	US-10-682-845-81	Sequence 81, Appl
38	956.5	75.0	495	10	US-09-948-004-18	Sequence 18, Appl
39	956.5	75.0	495	18	US-10-672-932-18	Sequence 18, Appl
40	956	74.9	281	14	US-10-112-788-9	Sequence 9, Appli
41	956	74.9	281	15	US-10-435-614-15	Sequence 15, Appl
42	950	74.5	438	14	US-10-244-821-88	Sequence 88, Appl
43	948.5	74.3	260	15	US-10-435-614-19	Sequence 19, Appl
44	941.5	73.8	423	14	US/10/013	Sequence 8, Appli
45	941.5	73.8	423	14	US/10/150	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-10-973-718-5

; Sequence 5, Application US/10973718

; Publication No. US20050214304A1

; GENERAL INFORMATION:

; APPLICANT: Pastan, Ira H.

; APPLICANT: Chowdhury, Partha S.

; APPLICANT: The Government of the United States

; APPLICANT: as represented by The Secretary of the

; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: Antibodies, Including Fv Molecules, and

; TITLE OF INVENTION: Immunconjugates Having High Binding Affinity for

; TITLE OF INVENTION: Mesothelin and Methods for Their Use

; FILE REFERENCE: 015280-339100US

; CURRENT APPLICATION NUMBER: US/10/973,718

; CURRENT FILING DATE: 2004-10-25

; PRIOR APPLICATION NUMBER: US/09/581,345

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: US 60/067,175

; PRIOR FILING DATE: 1997-12-01

; PRIOR APPLICATION NUMBER: WO PCT/US98/25270

; PRIOR FILING DATE: 1998-11-25

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 241

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:SS scFv

US-10-973-718-5

Query Match 99.8%; Score 1274; DB 18; Length 241;

Best Local Similarity 99.6%; Pred. No. 1.2e-82;

Matches	240;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	MOVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWKQSHGKSLIEWIGLITPYNGASS							60
Db	1	MOVQLQSGPELEKPGASVKISCKASGYSFTGYTMNWKQSHGKSLIEWIGLITPYNGASS							60
QY	61	YNQKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARGGYDGRGPDYWGQGTIVTSS							120
Db	61	YNQKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARGGYDGRGPDYWGQGTIVTSS							120
QY	121	GVGSGSGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQOKSGTSPKR							180
Db	121	GVGSGSGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQOKSGTSPKR							180
QY	181	WIYDTSKLASGVPGRRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI							240
Db	181	WIYDTSKLASGVPGRRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI							240
QY	241	K 241							
Db	241	K 241							

```

RESULT 2
US-10-259-087A-20
; Sequence 20, Application US/10259087A
; Publication No. US20030130190A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Ou, Shimian
; TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
; FILE REFERENCE: 1242/47/2
; CURRENT APPLICATION NUMBER: US/10/259,087A
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328123
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 2
US-10-259-087A-20

```

	Query Match	80.4%;	Score 1025.5;	DB 14;	Length 242;
	Best Local Similarity	81.7%;	Pred. No. 5.2e-65;		
	Matches 196;	Conservative 13;	Mismatches 30;	Indels 1;	Gaps 14;
QY	2 QVQLQQSGPELEKPGASVKLSCKAGSYFTGYTMNWVKQSHGSKLEWIGLITPYNGASSY	:	:	:	:
Db	3 QVKLQQSGPELVKPGASVKMSCKAGCYFTFSYVMHWKQKPGQGIEWIGINPNDGTKY	:	:	:	:
QY	62 NQFKRGKATLTVDKSSSTAYMDLLTSEDSAVFYFCARGYDGRFDYMGQTIVVSSG	:	:	:	:
Db	63 NEKFKGKALTSDKSSSTAYMEELSLTSEDSAAVYYCARFGNYG-ALDYWGQGTIVTVSSG	:	:	:	:
QY	122 VGGSGGGSGGGGSIDIELTQSPAIMSASPGEKYMTMTCASSSVSYMHWYQOKSGTSPKRW	:	:	:	:
Db	122 GGGSGGGSGGGGSIDIELTQSPITMASAPGEKVITTCASSSVSYMHWFQOKPGTSPKPW	:	:	:	:
QY	182 IYDTSKLASGVPRFSGSGSGNSYLTIISSVEAEADATYYCQQWSGYPLTFGAGTKLEIK	:	:	:	:
Db	182 IYGTSNLASGVPRFSGSGSGTYSILTISSMEAEADATYYCQQWSSYPPLTFGGGKTLEIK	:	:	:	:

```

RESULT 3
US-10-689-006-20
; Sequence 20, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Mernaugh, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72
; CURRENT APPLICATION NUMBER: US/10/689,006
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914,605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259,087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Artificial antibody ligand number 2
US-10-689-006-20

```

	Query Match	80.4%;	Score 1025.5;	DB 16;	length 242;
	Best Local Similarity	81.7%;	Pred. No. 5..2e-65;		
	Matches 196;	Conservative 13;	Mismatches 30;	Indels 1;	Gaps 1.;
QY	2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHKSLSEWIGLITPYNGASSY				61
Dd	3 QVKLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGGLEWIGIYNIDGTKY				62
QY	62 NQKFRGKATLTVDKSSSTAYMDLLSTSEBSAVYFCARGDGRGFDDYGQGTTVTVSSG				121
Dd	63 NEKFKGKALTSDKSSSTAYMELSLTSEBSAVYYCARFGNYG-ALDYWGQGTIVTVSSG				121
QY	122 VGGSGGGSGGGSDIELTSPAIMSASPGEKVMTCSASSSVSYMHWYQQRSGTSPKRW				181
Dd	122 GGGSGGGSGGGSDIELTSPTIMSASPGEKVITTCASSSVSYMHWFOQRGTSPKPW				181
QY	182 IYDTSKLASGVPRFSGSGGSYSLLTISSVEAEDDATYYYCQOWSGYPPLTFAGTKLEIK				241
Dd	182 IYGTSNLASGVPRFSGSGGSYSLLTISSWEAEDDATYYYCQOWSSYPPLTFGGGTKLEIK				241

```

RESULT 4
US-09-808-037-6
; Sequence 6, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON=2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-037-6

```

Query Match	79.2%;	Score 1010.5;	DB 9;	length 239;
Best Local Similarity	79.8%;	Pred. No. 5.9e-64;		
Matches 194;	Conservative 16;	Mismatches 26;	Indels 7;	Gaps 2;

DB 1 QVKLQESGAELVRPGVSVKISCKSGYFTDYAMHWMVKQSHAKSLEWIGVISTYYGDASY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLILTSSEDSAVYFCARG--GYDGRGFDYWGQGTTVTV 118
61 NQKFRGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116
QY 119 SSGVGGSGGGSGGSDIELTQSPAIMASAPGEKVTMTCSASSSVSYMHWYQOKSGTSP 178
117 SSGGGSGGVGSGGGSDIELTQSPAIMASAPGEKVTMTCSASSSISYMHWYQOKPGTSP 176
QY 179 KRWIYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYYCQOWSGYPLTFGAGTKL 238
177 KRWIYDTSKLASGVPARFSGSGSGTSLTISMEAEADATYYCHQRSSYPFTFGGAKL 236
QY 239 EIK 241
DB 237 EIK 239

RESULT 5
US-10-162-889-6
; Sequence 6, Application US/10162889
; Publication No. US2003007252A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: HANAN, Elia
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME
; TITLE OF INVENTION: USEFUL IN DIAGNOSING
; TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
; FILE REFERENCE: SOLOMON-2B
; CURRENT APPLICATION NUMBER: US/10/162, 889
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US/09/629, 971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473, 653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152, 417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-889-6

Query Match 79.2%; Score 1010.5; DB 14; Length 239;
Best Local Similarity 79.8%; Pred. No. 5.9e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;
QY 2 QVOLQSGPELEKPGASVKLSCKAGYSFTGYTMNWMVKQSHGKSLWIGLITPYNGASSY 61
DB 1 QVKLQESGAELVRPGVSVKISCKSGYFTDYAMHWMVKQSHAKSLEWIGVISTYYGDASY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLILTSSEDSAVYFCARG--GYDGRGFDYWGQGTTVTV 118
61 NQKFRGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116
QY 119 SSGVGGSGGGSGGSDIELTQSPAIMASAPGEKVTMTCSASSSVSYMHWYQOKSGTSP 178
117 SSGGGSGGVGSGGGSDIELTQSPAIMASAPGEKVTMTCSASSSISYMHWYQOKPGTSP 176
QY 179 KRWIYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYYCQOWSGYPLTFGAGTKL 238
177 KRWIYDTSKLASGVPARFSGSGSGTSLTISMEAEADATYYCHQRSSYPFTFGGAKL 236
QY 239 EIK 241
DB 237 EIK 239

RESULT 6

US-10-384-788-6
; Sequence 6, Application US/10384788
; Publication No. US20040013647A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A PLAQUE-FORMING DISEASE
; FILE REFERENCE: SOLOMON-2D.2
; CURRENT APPLICATION NUMBER: US/10/384, 788
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 60/371, 735
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 09/808, 037
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/830, 954
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 10/162, 889
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/473, 653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/629, 971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/152, 417
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/IL00/00518
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-788-6

Query Match 79.2%; Score 1010.5; DB 15; Length 239;
Best Local Similarity 79.8%; Pred. No. 5.9e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;
QY 2 QVOLQSGPELEKPGASVKLSCKAGYSFTGYTMNWMVKQSHGKSLWIGLITPYNGASSY 61
DB 1 QVKLQESGAELVRPGVSVKISCKSGYFTDYAMHWMVKQSHAKSLEWIGVISTYYGDASY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLILTSSEDSAVYFCARG--GYDGRGFDYWGQGTTVTV 118
61 NQKFRGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116
QY 119 SSGVGGSGGGSGGSDIELTQSPAIMASAPGEKVTMTCSASSSVSYMHWYQOKSGTSP 178
117 SSGGGSGGVGSGGGSDIELTQSPAIMASAPGEKVTMTCSASSSISYMHWYQOKPGTSP 176
QY 179 KRWIYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYYCQOWSGYPLTFGAGTKL 238
177 KRWIYDTSKLASGVPARFSGSGSGTSLTISMEAEADATYYCHQRSSYPFTFGGAKL 236
QY 239 EIK 241
DB 237 EIK 239

RESULT 7
US-10-618-856-6
; Sequence 6, Application US/10618856
; Publication No. US20040052766A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
; FILE REFERENCE: SOLOMON-2A
; CURRENT APPLICATION NUMBER: US/10/618, 856
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/473, 653A
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152, 417

; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-618-856-6

Query Match 79.2%; Score 1010.5; DB 15; Length 239;
Best Local Similarity 79.8%; Pred. No. 5.9e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
Db 1 QVKLQESGAELVPRGVSVKISCKSGYFTFDYAMHWVKQSHAKSLEWIGVISTYYGDASY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARG---GYDGRGFDYWGQGTITV 118
Db 61 NQKFRGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116
QY 119 SSGVGSGGGSGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYMHWYQOKSGTSP 178
Db 117 SSGGGSGGVSGGGSDIELTQSPAIMSASPEKVTMTCSASSSISYMHWYQOKPGTSP 176
QY 179 KRWIYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYYCQQWSGYPLTFGAGTKL 238
Db 177 KRWIYDTSKLASGVPARFSGSGSGTSTLTISMEAEDAATYYCHQRSSYPFTFGGAKL 236
QY 239 EIK 241
Db 237 EIK 239

RESULT 8
US-10-749-522-6
; Sequence 6, Application US/10749522
; Publication No. US20050089510A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: HANAN, Elia
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN DIAG
; FILE REFERENCE: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
; FILE REFERENCE: SOLOMON=2B
; CURRENT APPLICATION NUMBER: US/10/749,522
; CURRENT FILING DATE: 2004-01-02
; PRIOR APPLICATION NUMBER: US/09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-749-522-6

Query Match 79.2%; Score 1010.5; DB 17; Length 239;
Best Local Similarity 79.8%; Pred. No. 5.9e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
Db 1 QVKLQESGAELVPRGVSVKISCKSGYFTFDYAMHWVKQSHAKSLEWIGVISTYYGDASY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARG---GYDGRGFDYWGQGTITV 118
Db 61 NQKFRGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116
QY 119 SSGVGSGGGSGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYMHWYQOKSGTSP 178

Db 117 SSGGGSGGVSGGGSDIELTQSPAIMSASPEKVTMTCSASSSISYMHWYQOKPGTSP 176
QY 179 KRWIYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYYCQQWSGYPLTFGAGTKL 238
Db 177 KRWIYDTSKLASGVPARFSGSGSGTSTLTISMEAEDAATYYCHQRSSYPFTFGGAKL 236
QY 239 EIK 241
Db 237 EIK 239

RESULT 9
US-11-073-526-6
; Sequence 6, Application US/11073526
; Publication No. US20050152878A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: FRENKEL, Dan
; APPLICANT: HANAN, Elia
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN DIAG
; FILE REFERENCE: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
; FILE REFERENCE: SOLOMON=2C
; CURRENT APPLICATION NUMBER: US/11/073,526
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/830,954
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: PCT/IL00/00518
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-526-6

Query Match 79.2%; Score 1010.5; DB 20; Length 239;
Best Local Similarity 79.8%; Pred. No. 5.9e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
Db 1 QVKLQESGAELVPRGVSVKISCKSGYFTFDYAMHWVKQSHAKSLEWIGVISTYYGDASY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARG---GYDGRGFDYWGQGTITV 118
Db 61 NQKFRGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116
QY 119 SSGVGSGGGSGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYMHWYQOKSGTSP 178
Db 117 SSGGGSGGVSGGGSDIELTQSPAIMSASPEKVTMTCSASSSISYMHWYQOKPGTSP 176
QY 179 KRWIYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYYCQQWSGYPLTFGAGTKL 238
Db 177 KRWIYDTSKLASGVPARFSGSGSGTSTLTISMEAEDAATYYCHQRSSYPFTFGGAKL 236
QY 239 EIK 241
Db 237 EIK 239

RESULT 10
US-10-689-006-24
; Sequence 24, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:


```

; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scfv EPCAMxCD3 with M4 mutant in anti-CD3 part
US-10-682-845-63

```

Query Match	75.8%;	Score 967.5;	DB 16;	Length 492;
Best Local Similarity	77.3%;	Pred. No. 1.4e-60;		
Matches 187; Conservative	17;	Mismatches 35;	Indels 3;	Gaps 1;

QY	3	VOLQOOGPELEKPGASVKLSCKASGYSTGYTMNWKQSHGKSLIEWIGLITPYNGASSTN	62
		::: : : : : : : : : : :	
Db	245	IKLQOGAEIARPGASVKMSCKTSGYTFTRYTMHWKQRPQGLEWIGINPSRGYTNN	304
QY	63	QKFRGKATLTVDKSSSTAYMDLISLTSEDSAVVFCARGGYDGRGFDYWGQGTVTVAS--	120
		: : : : : : : : : :	
Db	305	QKFKDKATLTLDKSSSTAYMQLSSLTSEDSAVVYCYARYSDHICYLDYWGQGTTLTVSSVE	364
QY	121	-GVGSGGGSGGSGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQOKSGTSPK	179
		: : : : : : : : : :	
Db	365	GSGSGSGSGSGGVDIQLTQSPAIMSASPGEKVTMTCRASSSVSYMHWYQOKSGTSPK	424
QY	180	RMWYDTSKLASGVPRFSGSGSGNSYSLTISVEAEDDATYYCQOWSGYPLTFGAGTKLE	239
		: : : : : : : : : :	
Db	425	RMWYDTSKVASGVPRFSGSGSGTSLTISMEAEADATYYCQOWSNPLTFGAGTKLE	484

QY	240	IK	241
	:		
Db	485	LK	486

```

RESULT 14
US-10-682-845-79
; Sequence 79, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAMxCD3 with M31 mutant in anti-CD3 part
US-10-682-845-79

```

Query Match	75.8%;	Score 967.5;	DB 16;	Length 492;
Best Local Similarity	77.8%;	Pred. No. 1.4e-60;		
Matches 189; Conservative	18;	Mismatches 31;	Indels 5;	Gaps 3;

```

QY      3 VQLOOSGPELEKPGASVYKLSCKASGYSFTGYTMNMWVKQSHKSLWIGLITPYNGASSYN 62
      ::||||| | : |||||::||| |||: ||| | : ||||| | : |||
Db      245 IKQOOSGAELARPGASVYMSCKTSGYTFIRYTMHWVKQRPQOGLWIGYINPSRGYTNYN 304

```

[illegible]

```

RESULT 15
US-10-682-845-83
; Sequence 83, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682, 845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAMxCD3 with M65 mutant in anti-CD3 part
US-10-682-845-83

```

[illegible]

Search completed: October 24, 2005, 20:20:03
Job time : 167 secs